

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 22:35:16 ; Search time 232 seconds
(without alignments)
964.019 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGGVRTALALILG.....MFSYPSLYPPFYGAEPH 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1730	100.0	317	1 SFRP5_HUMAN	Q514F7 homo sapien
2	1656	95.7	315	1 SFRP5_BOVIN	Q9XCI1 bos taurus
3	1613	93.2	314	1 SFRP5_MOUSE	Q9W966 mus musculu
4	1160.5	67.1	315	2 O6GI50_XENTR	Q6GI50 xenopus tro
5	1157.5	66.9	315	2 O8AWG4_XENLA	Q8AWG4 xenopus lae
6	1155.5	66.8	315	2 O640J3_XENLA	Q640J3 xenopus lae
7	1104.5	63.8	321	2 O4SKC3_TETNG	Q4SKC3 tetradon n
8	1089	62.9	310	2 O6VNR8_BRARE	Q6VNR8 brachydano
9	924.5	53.4	314	1 SFRP1_HUMAN	Q8N474 homo sapien
10	910.5	52.6	308	1 SFRP1_BOVIN	O19116 bos taurus
11	909	52.5	314	2 O505A2_MOUSE	Q505A2 mus musculu
12	903	52.2	314	1 SFRP1_MOUSE	Q8CAU3 mus musculu
13	851	49.2	306	2 O6GZK1_ORYLA	Q6GZK1 oryzae lat
14	838	48.4	314	1 SFRP1_CHICK	Q9G4K1 gallus gall
15	836.5	48.4	311	2 O9Y124_XENLA	O9Y124 xenopus lae
16	802	46.4	296	2 O7TK9_BRARE	Q7TK9 brachydano
17	783	45.3	281	2 O568X0_BRARE	Q568X0 brachydano
18	744	43.0	311	2 O8JHC7_BRARE	Q8JHC7 brachydano
19	712	41.2	282	2 O8JHC7_BRARE	Q8JHC7 brachydano
20	672	38.8	295	2 O4SS00_TETNG	Q4SS00 tetradon n
21	643	37.2	295	2 O6PAB8_XENTR	Q6PAB8 xenopus tro
22	643	37.2	298	2 O7ZXM6_XENLA	Q7ZXM6 xenopus lae
23	620.5	35.9	295	1 SFRP2_MOUSE	P97299 mus musculu
24	617	35.7	294	1 SFRP2_CANPA	Q96311 canis famli
25	616	35.6	283	2 O9BGB6_RABIT	Q9BGB6 cryptocolag
26	614.5	35.5	295	1 SFRP2_HUMAN	Q9B6F1 homo sapien
27	602	34.8	292	1 SFRP2_CHICK	Q91396 gallus gall
28	581	33.6	365	2 O4H2U5_CIOIN	O4H2U5 ciona intes
29	568.5	32.9	300	2 O6FZB8_XENTR	Q6FZB8 xenopus tro
30	568	32.8	307	2 O42397_CHICK	O42397 gallus gall
31	564.5	32.6	295	2 O91897_XENLA	O91897 xenopus lae

32	490.5	28.4	293	2	Q4H2U4_CIOIN	Q4H2U4 ciona intes
33	473	27.3	115	2	Q90ZG6_BRARE	Q90ZG6 brachydano
34	453	26.2	158	1	SFRP1_RAT	Q9168 ratuus norv
35	431	24.9	282	2	Q4RS17_TETNG	Q4RS17 tetradon n
36	398	23.0	280	2	O91AUS_XENLA	O91AUS xenopus lae
37	396.5	22.9	261	2	O61U61_CABER	O61U61 caenorhadi
38	396	22.9	281	2	O73821_XENLA	O73821 xenopus lae
39	390.5	22.6	284	2	O90ZAG_AMBME	Q90ZAG ambystoma m
40	388	22.4	260	2	O9GUF5_CABEL	Q9GUF5 caenorhadi
41	373	21.6	178	2	O6ZSL4_HUMAN	O6ZSL4 homo sapien
42	370.5	21.4	282	2	O7SX78_BRARE	O7SX78 brachydano
43	370.5	21.4	289	2	O504U9_BRARE	O504U9 gallus gall
44	300	17.3	567	1	F2D7_CHICK	O57329 gallus gall
45	292.5	16.9	574	1	F2D7_HUMAN	O75084 homo sapien

ALIGNMENTS

RESULT 1
ID SFRP5_HUMAN STANDARD; PRT; 317 AA.
AC Q514F7; O14780; Q86TH7;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Secreted frizzled-related protein 5 precursor (SFRP-5) (Secreted apoptosis related protein 3) (SARP-3) (Frizzled-related protein 1b) (FRP-1b).
GN Name=SFRP5; Synonyms=FRP1b, SARP3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=pancreas;
RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M., Fitzpatrick P.A., Kiefer M.C., Tomei L.D., Umaneky S.R.;
RT "SARPs: a family of secreted apoptosis-related proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX PubMed=9642116; DOI=10.1006/birc.1998.8784;
RA Hu E., Zhu Y., Fredrickson T., Barnes W., Kelsell D., Bealey L., Brooks D.;
RT "Tissue restricted expression of two human Frzbs in preadipocytes and pancreas.";
RL Biochem. Biophys. Res. Commun. 247:287-293(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=retina;
RX PubMed=10072424; DOI=10.1093/hmg/8.4.575;
RA Chang J.T., Gami N., Moore K., Li Y., Zhang S., Chew C., Goodman B., Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 8:575-583(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT GLY-7.
RC TISSUE=retal brain;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization.";
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANT GLY-7.
RX PubMed=15164054; DOI=10.1038/nature02462;
RA Deloukas P., Barthrowl M.E., Grafham D.V., Rubinfeld M., French L., Steward C.A., Sims S.K., Jones M.C., Seale S., Scott C., Howe K., Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L., Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P.,

RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baguley C.L., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
 RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Corry N., Coulson A., Dhumi P., Dutta I., Dunn M., Faulkner L.,
 RA Grifflith A., Frankland J.A., Garner P., Garnett S., Griddle S.,
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McIay K.E., McWherry A.,
 RA Mshreghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Lacey E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Pelen S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarrifidou T., Sehra H.K., Showkhen R., Skuce C.D., Smith M.,
 RA Stauding L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 RA Tracey A., Tromans A., Tsolas J., Wall M., Walsh J., Wang H.,
 RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Siebert R., Fochtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.,
 RA "The DNA sequence and comparative analysis of human chromosome 10,"
 RA Nature 429:375-381 (2004).

RT [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=BNS;

RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stalcenon M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Garunci P., Prance C.,

RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,

RA Bosak S.A., McMan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,

RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marz M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Soluble frizzled-related proteins (SFRPs) function as

CC modulators of Wnt signaling through direct interaction with Wnts.

CC They have a role in regulating cell growth and differentiation in

CC specific cell types. SFRPs may be involved in determining the

CC polarity of photoreceptor, and perhaps, other cells in the retina.

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- TISSUE SPECIFICITY: Highly expressed in the retinal pigment

CC epithelium (RPE) and pancreas. Weak expression in heart, liver and

CC muscle.

CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By

CC similarity).

CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein

CC (SFRP) family.

CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.

CC -1- SIMILARITY: Contains 1 NTR domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

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CC use as long as its content is in no way modified and this statement is not

CC removed.

DR EMBL, AL358938; CA114274.1; -; Genomic_DNA.

DR EMBL, BC050435; AAH50435.2; -; mRNA.

DR PIR, J01075; J01075.

DR HSSP, 061091; 11Y7.

DR Ensembl, ENSG00000120057; Homo sapiens.

DR HGNC, HGNC:10779; SFRP5.

DR MIM, 604158; -; SFRP5.

DR InterPro, IPR000024; Fz domain.

DR InterPro, IPR01134; Netrin_C.

DR Pfam, PF01392; Fz, 1.

DR Pfam, PF01759; NTR, 1.

DR SMART, SM00643; C345C; 1.

DR SMART, SM00063; FRI, 1.

DR PROSITE, PS50038; FZ, 1.

DR PROSITE, PS50189; NTR, 1.

KW Developmental protein; Differentiation; Polymorphism; Signal;

KW Wnt signaling pathway.

FT SIGNAL 1 29

FT CHAIN 30 317

FT DOMAIN 48 165

FT DISULFID 181 303

FT DISULFID 53 116

FT DISULFID 63 109

FT DISULFID 100 135

FT DISULFID 124 162

FT DISULFID 128 152

FT DISULFID 181 255

FT DISULFID 184 253

FT DISULFID 198 303

FT VARIANT 7 7

FT CONFLICT 33 33

FT SQ SEQUENCE 317 AA; 35577 MW; 05F1FCCB614F36A CRC64;

Query Match

Best Local Similarity 100.0%; Score 1730; DB 1; Length 317;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRAAAAGGVTATLALLLGLAHVAPARCEEDYVWQAEPLHGRHSYKSPQCDIPADL 60

1 MRAAAAGGVTATLALLLGLAHVAPARCEEDYVWQAEPLHGRHSYKSPQCDIPADL 60

61 PLCHTVGKRRKRLPVLHESLAEVKQOASSMLPLAKRGHSDTVFLCSLPAPVCLDRP 120

61 PLCHTVGKRRKRLPVLHESLAEVKQOASSMLPLAKRGHSDTVFLCSLPAPVCLDRP 120

121 IYPCRSLEAVRAGCAPLMEAYGFPVPMILCHKRLPNDICIAVQFGLPATAPVTKI 180

121 IYPCRSLEAVRAGCAPLMEAYGFPVPMILCHKRLPNDICIAVQFGLPATAPVTKI 180

181 CAOCMEHSADGLMEQWCSDFVVMRIKEIKIENGDRKLGAOKKKLLKRGPLKRDY 240

181 CAOCMEHSADGLMEQWCSDFVVMRIKEIKIENGDRKLGAOKKKLLKRGPLKRDY 240

241 KRLVLMKMGAGCCPQPLDSLAGSFLVNGRVDGLLMAVYRMDKKNKKFAVKFMS 300

241 KRLVLMKMGAGCCPQPLDSLAGSFLVNGRVDGLLMAVYRMDKKNKKFAVKFMS 300

301 YPCSLYPPFPYGAABPH 317

301 YPCSLYPPFPYGAABPH 317

RESULT 2

SFRP5_BOVIN

ID SFRP5_BOVIN STANDARD; PRT; 315 AA.

AC Q9XSC1;

DT 10-MAY-2005 (Rel. 47, Created)

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

GN Secreted frizzled-related protein 5 precursor (SFRP-5).

GN Name=SFRP5.

OS Bos taurus (Bovine).

CC (eRRP) family.
 CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AF117759; AAD25053.1; -; mRNA.
 DR EMBL: BC032921; AAH32921.1; -; mRNA.
 DR HSSP: OG1091, 110Y.
 DR MGI: MGI:1860298; Strps.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR InterPro: IPR000024; Fz domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00643; C34SC; 1.
 DR SMART: SM00643; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 DR PROSITE: PS50189; NTR; 1.
 DR Developmental protein; Differentiation; Signal; Wnt signaling pathway.
 KW SIGNAL
 FT CHAIN 1 21 Potential.
 FT CHAIN 2 21 Secreted frizzled-related protein 5.
 FT DOMAIN 45 162 FZ.
 FT DOMAIN 178 300 NTR.
 FT DISULFID 50 113 By similarity.
 FT DISULFID 60 106 By similarity.
 FT DISULFID 97 132 By similarity.
 FT DISULFID 121 159 By similarity.
 FT DISULFID 125 149 By similarity.
 FT DISULFID 178 250 By similarity.
 FT DISULFID 181 252 By similarity.
 FT DISULFID 195 300 By similarity.
 FT CONFLICT 128 128 A -> V (in Ref. 2).
 SQ SEQUENCE 314 AA; 35382 MW; 296847F56D1CAFDD CRC64;
 Query Match 93.2%; Score 1613; DB 1; Length 314;
 Best Local Similarity 94.9%; Pred. No. 7,2e-139;
 Matches 295; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 7 AGCVRTAALALLGALHMAPARCEVDYDYGMAEPLHGRSYKPPQCLDIPADLPCHTV 66
 DB 4 AMSASTAALALLGALHGAPTRGQEDYDYGMAEPLHGRSYKPPQCLDIPADLPCHTV 63
 QY 67 GYKRMRLPVLHESLAEVKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIYPCRS 126
 DB 64 GYKRMRLPVLHESLAEVKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIYPCRS 123
 QY 127 LCEAVRAGCAPLMEAYGFPWPEMLHCHKEPRLDNDLCIAVQFGLPATAVPYTKIQAQCEM 186
 DB 124 LCEAVRAGCAPLMEAYGFPWPEMLHCHKEPRLDNDLCIAVQFGLPATAVPYTKIQAQCEM 183
 QY 187 EHSADGLMEQWSSDFVVMRIKEIKIENGDRKLTGAQKKKLLKPGPKRDTKRLVLA 246
 DB 184 EHSADGLMEQWSSDFVVMRIKEIKIENGDRKLTGAQKKKLLKPGPKRDTKRLVLA 243
 QY 247 MNGAGCPCPOLDSLAFSLVMGRKVDGOLLMAVYRMDKKNKEMKEAFKMEFSYPCSLX 306
 DB 244 MNGAGCPCPOLDSLAFSLVMGRKVDGOLLMAVYRMDKKNKEMKEAFKMEFSYPCSLX 303
 QY 307 YPFFYGAAEPH 317
 DB 304 YPFFYGAAEPH 314

RESULT 4
 O6GL50_XENTR PRELIMINARY; PRT; 315 AA.
 O6GL50_XENTR AC
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGCE9423 protein.
 GN Name=MGCE9423;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 OX NCBI_TaxID=8364;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marulanda K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield A.S.N., Krzywinski M.I., Skalske U., Smallov D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo.
 RP Klein S., Gerhardt D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC074661; AAH74661.1; -; mRNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO: GO:0007275; P:development; IEA.
 DR GO: GO:0016055; P:receptor signaling pathway; IEA.
 DR InterPro: IPR000024; Fz domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01759; NTR; 1.
 DR Pfam: PF01392; Fz; 1.
 DR SMART: SM00643; C34SC; 1.
 DR SMART: SM00643; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 DR PROSITE: PS50189; NTR; 1.
 SQ SEQUENCE 315 AA; 36455 MW; 9DB8E912FB3A386 CRC64;
 Query Match 67.1%; Score 1160.5; DB 2; Length 315;
 Best Local Similarity 70.0%; Pred. No. 1.7e-97;
 Matches 203; Conservative 47; Mismatches 37; Indels 3; Gaps 2;

QY 16 ALLGALHMAPARCEVDYDYGMAEPLHGRSYKPPQCLDIPADLPCHTVGYKRMRLP 74
 DB 13 SLILGLVMSGA--BEVYYISQWQNDNPNQNGFYTKQSCIDIPSDLHCHVAVYKXKRLP 70
 QY 75 NILHESLAEVKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIYPCSLCEAVYAG 134
 DB 71 NILDHETMPEVYKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIYPCSLCEAVYAG 130
 QY 135 CAPLMEAYGFPWPEMLHCHKEPRLDNDLCIAVQFGLPATAVPYTKIQAQCEMSADGLM 194
 DB 131 CAPVMEISYGFPMPEMLHCHKEPRLDNDLCITVQFSGKQYTPPVYTKIQAQCEMSADGLM 190
 QY 195 EOMCSDFVVMRIKEIKIENGDRKLTGAQKKKLLKPGPKRDTKRLVLAHMGAGACP 254
 DB 191 VQLCASDVLVLMRIKEIKIENGDRKLTGAQKKKLLKPGPKRDTKRLVLAHMGAGACP 250

QY 255 CPQDLNLSGSLVWGRKVDGOLLMAVYRMDKKNKEMKFAVPMFSPCS 304
 DB 251 CPQDLNLSGSLVWGRKVDNKLTLTAIYKMDKSKDMKAVANPMFSPCS 300

RESULT 5

Q8AWG4 XENLA PRELIMINARY; PRT; 315 AA.

AC Q8AWG4; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Secured frizzled-related protein 5.
 GN Name=FRP5;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=83355;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22505169; PubMed=12617827; DOI=10.1016/S1567-133X(02)00023-6;
 RA Pilcher K.B., Kriegl P.A.;
 RT "Expression of the Wnt inhibitor, sFRP5, in the gut endoderm of
 RT Xenopus.";
 RL Gene Expr. Patterns 2:369-372(2002).
 DR EMBL; AY164461; AAN87352.1; -; mRNA.
 DR HSSP; 061091; 110Y.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0016055; P:Wnt receptor signaling pathway; IEA.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01759; NTR; 1.
 DR SMART; SM00643; C34SC; 1.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50189; NTR; 1.
 SQ SEQUENCE 315 AA; 36441 MW; 208E7706AC9ED431 CRC64;

Query Match 66.9%; Score 1157.5; DB 2; Length 315;
 Best Local Similarity 69.7%; Pred. No. 3.2e-97;
 Matches 202; Conservative 48; Mismatches 37; Indels 3; Gaps 2;

QY 16 ALLGALHMAPRCEBYDYWGQAEPL-HGRSYKPPQCLDIPADLPICHTVGYKRMRLP 74
 DB 13 SVTLGLVWMSA--EEYDYYSQSDNFPQGRFYTKSQSCIDIPSDIHLCHNVGYKMRLLP 70
 QY 75 NILHESLAEVYQQAQSSWPLILAKRCHSDTOVFLCSLPAFVCLDPRIPYCRSLCEAVRAG 134
 DB 71 NILDHEIPEVYQQAQSSWVPLILAKRCHSDTOVFLCSLPAFVCLDPRIPYCRSLCEAVRDS 130
 QY 135 CAPLMEAYGFPMPEMLHGHFPLDNDLCTAVOGFHLPATAPYPTKCAQCEMEHSADGLM 194
 DB 131 CAPWESYGFPMPEMLHGHFPLDNDLCTAVOGFHLPATAPYPTKCAQCEMEHSADGLM 190
 QY 195 EQMGSGDFVVKRIKIKIENGDRKILGAQKKKKLLKPPILKPKDKTKRLVLMKNGACGP 254
 DB 191 VQLCASDFVLRIRIKIKIENGDRKILGAQKKKKLLKPPILKPKDKTKRLVLMKNGACGP 250
 QY 255 CPQDLNLSGSLVWGRKVDGOLLMAVYRMDKKNKEMKFAVPMFSPCS 304
 DB 251 CPQDLNLSGSLVWGRKVDNKLTLTAIYKMDKSKDMKAVANPMFSPCS 300

RESULT 6

Q64003 XENLA PRELIMINARY; PRT; 315 AA.

AC Q64003; 25-OCT-2004 (Tremblrel. 28, Created)
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
 DB LOC494659 protein.
 GN Name=LOC494659;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=83355;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Scheetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman D.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Scheetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman D.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

Query Match 66.8%; Score 1155.5; DB 2; Length 315;
 Best Local Similarity 69.7%; Pred. No. 4.8e-97;
 Matches 202; Conservative 48; Mismatches 37; Indels 3; Gaps 2;

QY 16 ALLGALHMAPRCEBYDYWGQAEPL-HGRSYKPPQCLDIPADLPICHTVGYKRMRLP 74
 DB 13 SVTLGLVWMSA--EEYDYYSQSDNFPQGRFYTKSQSCIDIPSDIHLCHNVGYKMRLLP 70
 QY 75 NILHESLAEVYQQAQSSWPLILAKRCHSDTOVFLCSLPAFVCLDPRIPYCRSLCEAVRAG 134
 DB 71 NILDHEIPEVYQQAQSSWVPLILAKRCHSDTOVFLCSLPAFVCLDPRIPYCRSLCEAVRDS 130

QY 135 CAPLMEAYGFPMPEMLHCHKFPDLNDLCIAVOFGHLPATAPVYTKICAOCEMEHSADGLM 194
 DB 131 CAPVMESSYGFPMPEMLNCKFPDLNDLCITVQFGSKQVQTPVPTIKICTQCEITEOKSEYTR 190
 QY 195 EOMGSSDFVKKRIKEIKIENGDRKLIGAKKKKLLKQGPLKRTKTLVLMKKGAGCP 254
 DB 191 VOLCSDPFLRRIRKEIKIENGDRKLIAQKKKKKLLKQKKLKRKKEFRKLVLTKNAASCP 250
 QY 255 CPQDLSLAGFLVMGRKYDGOQLLMAVYRWDKKNKEMKFAVMEFSPCS 304
 DB 251 CPQDNLNLSGSLIMGRKYDKNKILAIYKMDKSKSDMKAYVFMFSTYPCS 300

RESULT 7
 Q4SKX3 TETNG
 ID Q4SKX3 TETNG PRELIMINARY; PRT; 321 AA.

AC 04SKX3
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Chromosome 17 SCAF14563, whole genome shotgun sequence.
 DE (Fragment).
 CN ORFNames=GSTENG00016514001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NC NCBI_Taxid=99863;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bounau D., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Flier S., Lutfalla G., Dossat C., Segurens B.,
 RA Daelva C., Salanoubat M., Levy M., Boudet N., Castellan S.,
 RA Anthouard V., Juhn C., Caetelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Catolico L., Poulin J., De Berardinis V.,
 RA Criard C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chaplie C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Landier E.S., Weissenbach J., Roest Crolious H.,
 RA RT the early vertebrate proto-karyotype.";
 RA Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAEB01014563; CAF98709.1; -; Genomic_DNA.
 FT NON TER 321
 SQ SEQUENCE 321 AA; 36657 MW; 3060A2F9AD478156 CRC64;

Query Match 63.8%; Score 1104.5; DB 2; Length 321;
 Best Local Similarity 65.9%; Pred. No. 2.3e-92;
 Matches 201; Conservative 41; Mismatches 58; Indels 5; Gaps 2;
 QY 7 AGGVTAAATLALGALHWAAPACEEDYGYMAEPHL-GRSYSKPQCLIDIPADLPCHT 65
 DB 20 APLGSLVPSLLILLITVSA----DEYDYYSWQSDNPFHNGRFYTKQPCQCDIVDRLCHN 75
 QY 66 VGYKMRLLPNLLEHSLAEVKKQASWMLFLAKRGCHSDTQVFLGSLFAPVCLDRIRYPCR 125
 DB 76 VGYKMRLLPNLLEHSLAEVKKQASWMLFLAKRGCHSDTQVFLGSLFAPVCLDRIRYPCR 135
 QY 126 SLCEAVRAGCAPLMEAYGFPMPEMLHCHKFPDLNDLCIAVOFGHLPATAPVYTKICAOCE 185
 DB 136 SLCEAVRAGCAPLMEAYGFPMPEMLHCHKFPDLNDLCIAVOFGHLPATAPVYTKICAOCE 195

QY 186 MEHSADGLMEOMCSSDFVKKRIKEIKIENGDRKLIGAKKKKLLKQGPLKRTKTLVL 245
 DB 196 NELRADNIMTEHYCASDFALKKRIKEVKKENKDRKLIAQKKKKYIKUGALFKKDLKLT 255
 QY 246 HMKKGAGPCQDLSLAGFLVMGRKYDGOQLLMAVYRWDKKNKEMKFAVMEFSPCS 305
 DB 256 YIKGANCPCQDLSLAGFLVMGRKYDGOQLLMAVYRWDKKNKEMKFAVMEFSPCS 315
 QY 306 YYPEF 310
 DB 316 YHTVF 320

RESULT 8
 Q6YNR8 BRARE
 ID Q6YNR8 BRARE PRELIMINARY; PRT; 310 AA.

AC Q6YNR8
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Secreted fibrinogen-related protein 1 (Secreted fibrinogen-related protein 5).
 DE
 CN Name=sfrp5; Synonyms=frpl;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_Taxid=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Shin J., Kim S.H., Yeo S.Y., Huh T.L.;
 RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Larvae;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda N.B., Toshimiki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Larvae;
 RG NIH MC Project;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050560; AAH11439.1; -; mRNA.
 DR EMBL; BC085455; AAH85455.1; -; mRNA.
 DR ZFIN; ZDB-GENE-011108-2; sfrp5.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0016055; P:ant receptor signaling pathway; IEA.
 DR InterPro; IPR000124; Fz domain.
 DR InterPro; IPR00134; Netrin_C.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01759; NTR; 1.
 DR SMART; SM00643; C345C; 1.

DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50189; NTR; 1.
 SO SEQUENCE 310 AA; 35393 MW; 77D3412C6CCCE8EA4 CRC64;
 Query Match 62.9%; Score 1089; DB 2; Length 310;
 Best Local Similarity 65.7%; Pred. No. 5.7e-91;
 Matches 197; Conservative 41; Mismatches 56; Indels 6; Gaps 2;
 QY 12 TAAATLLGALHAPARCEERYDYGYGQAEPLH-GRGSRKPPQCLDIPADLPCHTGYGR 70
 DB 15 TLALVLTSA-----SSAEYDYYSWQSDHFSGRFRYAKQPPQVDIPADIRLTYNVGYKK 69
 QY 71 MRLPNLLEHESLAEVQQAQASWMLPLAKRCHSDTOYFSLSPAPVCLDRPIYCRSLCEA 130
 DB 70 MRLPNLIDHETMEVQQAQASWMLPLAKRCHADTOYFSLSPAPVCLDRPIYCRSLCEA 129
 QY 131 VRAGCAPLMEAYGPPPEPMILHCKHPLNDLCLAVQFGLPATAPPVTKI CAOCMEHSA 190
 DB 130 VEDSCAPVMEYGFPPPEMLQCEKFPIDNLCIPMOFSAHATQTVFSKVCPCDWELXA 189
 QY 191 DGLMEQCSDFVYKRIKIKIENGDRKLGAKKKKLLKPKKDKRKLVIAMKNG 250
 DB 190 DTLMEHYCASDFALKMKIKKAKKEGDRKLIQAQKKKVLKMGILKDKDKLTLTKNG 249
 QY 251 AGCPCPQLDSLAFVVMGRKRVGOLLMAVVMKDKKEMKFAVFMESYPCSLYYPPF 310
 DB 250 ANCPGQDLNLGSLFIMGRKRVQOLLMSIHMDKSKSLKALIKYISQCPPTYHSVF 309
 RESULT 9
 SFRP1 HUMAN
 ID SFRP1 HUMAN STANDARD; PRT; 314 AA.
 AC Q8N474; O00546; 014779;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Secreted frizzled-related protein 1 precursor (SFRP-1) (Frizzled-related protein 1) (FRP-1) (Secreted apoptosis-related protein 2) (SARP-2).
 OS Homo sapiens (Human).
 GN Name=SFRP1; Synonyms=FRP, FRP1, SARP2;
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 39-78.
 RP TISSUE=Embryonic lung fibroblast;
 RA MEDLINE=97338093; PubMed=9192640; DOI=10.1073/pnas.94.13.6770;
 RA Finch P.W., He X., Kelley M.J., Uren A., Schaudies R.P., Popescu N.C., Rudloff S., Aaronson S.A., Varnus H.E., Rubin J.S.;
 RT "Purification and molecular cloning of a secreted, frizzled-related antagonist of Wnt action.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:6770-6775 (1997).
 RN [2]
 RC NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 RP TISSUE=Heart;
 RA MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
 RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M., Fitzpatrick P.A., Klefer M.C., Tomei L.D., Unanue S.R.;
 RT "SARPs: a family of secreted apoptosis-related proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641 (1997).
 RN [3]
 RC NUCLEOTIDE SEQUENCE [MRNA], AND INDUCTION.
 RP PubMed=9724099;
 RA Zhou Z., Wang J., Han X., Zhou J., Linder S.;
 RT "Up-regulation of human secreted frizzled homolog in apoptosis and its down-regulation in breast tumors.";
 RT Int. J. Cancer 78:95-99 (1998).
 RN [4]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Brain;

RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP PROTEIN SEQUENCE OF 32-314, DISULFIDE BONDS, MASS SPECTROMETRY,
 N-LINKED GLYCOSYLATION, AND MUTAGENESIS OF ASN-173 AND ASN-263.
 RX PubMed=11741940; DOI=10.1074/jbc.M108533200;
 RA Chong J.M., Ueren A., Rubin J.S., Spetcher D.W.;
 RT "Disulfide bond assignments of secreted frizzled-related protein-1 provide insights about frizzled homology and netrin modules.";
 RT J. Biol. Chem. 277:5134-5144 (2002).
 RN [6]
 RP INTERACTIONS WITH WNT1, WNT2 AND FRZ6.
 RX PubMed=10347172; DOI=10.1074/jbc.274.23.16180;
 RA Bafico A., Gazit A., Premila T., Finch P.W., Yaniv A., Aaronson S.A.;
 RT "Interaction of frizzled related protein (FRP) with Wnt ligands and the frizzled receptor suggests alternative mechanisms for FRP inhibition of Wnt signaling.";
 RT J. Biol. Chem. 274:16180-16187 (1999).
 RN [7]
 RP INDUCTION.
 RX PubMed=11932307; DOI=10.1210/jc.87.4.1729;
 RA Fukushima K., Kariya M., Kita M., Shine H., Kanamori T., Kosaka C., Orii A., Fujita J., Fujii S.;
 RT "Secreted frizzled related protein 1 is overexpressed in uterine leiomyomas, associated with a high estrogenic environment and unrelated to proliferative activity.";
 RT J. Clin. Endocrinol. Metab. 87:1729-1736 (2002).
 CC [1-] FUNCTION: Soluble frizzled-related proteins (SFRPs) function as modulators of Wnt signaling through direct interaction with Wnt5. They have a role in regulating cell growth and differentiation in specific cell types. SFRP1 decreases intracellular beta-catenin levels (By similarity). Has antiproliferative effects on vascular cells, in vitro and in vivo, and can induce, in vivo, an angiogenic response. In vascular cell cycle, delays the G1 phase and entry into the S phase (By similarity). In kidney development, inhibits tubule formation and bud growth in metanephros (By similarity). Inhibits WNT1/WNT4-mediated TGF-dependent transcription.
 CC [1-] SUBUNIT: Interacts with WNT1, WNT2 and FRZ6. Interacts with WNT4 and WNT8 (By similarity).
 CC [1-] SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular matrix-associated. Released by heparin-binding.
 CC [1-] TISSUE SPECIFICITY: Widely expressed. Absent from lung, liver and peripheral blood leukocytes. Highest levels in heart and fetal kidney. Also expressed in testis, ovary, fetal brain and lung, leiomyoma cells, myometrial cells and vascular smooth muscle cells. Expressed in foreskin fibroblasts and in keratinocytes.
 CC [1-] INDUCTION: Down-regulated in colorectal and breast tumors. Up-regulated in uterine leiomyomas under high estrogenic conditions. Expression, in leiomyoma cells, also increased both under hypoxic and serum deprivation conditions.
 CC [1-] DOMAIN: The FZ domain is involved in binding with Wnt ligands (By similarity).
 CC [1-] MASS SPECTROMETRY: MW=7266.4; METHOD=MALDI; RANGE=169-210;

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CC NOTE=Isoform N-glycosylated on Asn-173 (Ref.5).
CC -1- MISCELLANEOUS: May have therapeutic use in cardiac surgery.
CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
CC (sFRP) family.
CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AF001900; AAB61576.1; -; mRNA.
DR EMBL, AF017987; AAB70793.1; -; mRNA.
DR EMBL, AF056087; AAC12877.1; -; mRNA.
DR EMBL, BC036503; AAB36503.1; -; mRNA.
DR HSSP, Q61091; 110Y.
DR Ensembl, ENSG00000104332; Homo sapiens.
DR HGNC, HGNC:10776; SFRP1.
DR MIM, 604156; -.
DR InterPro, IPR000024; Fz domain.
DR InterPro, IPR001134; Netrin_C.
DR Pfam, PF01392; Fz; 1.
DR Pfam, PF01759; NTR; 1.
DR SMART, SM00643; C345C; 1.
DR SMART, SM00063; FRL; 1.
DR PROSITE, PSS0038; FZ; 1.
DR PROSITE, PSS0189; NTR; 1.
KW Developmental protein; Differentiation; Direct protein sequencing;
KW Glycoprotein; Signal; Wnt signaling pathway.
FT SIGNAL 1 31
FT CHAIN 32 314
FT DOMAIN 53 169
FT DOMAIN 186 306
FT CARBOHYD 173 173
FT DISULFID 58 121
FT DISULFID 68 114
FT DISULFID 105 140
FT DISULFID 129 166
FT DISULFID 133 157
FT DISULFID 186 236
FT DISULFID 189 258
FT DISULFID 203 306
FT MUTAGEN 173 173
FT MUTAGEN 263 263
FT CONFLICT 14 14
FT CONFLICT 174 174
SQ SEQUENCE 314 AA; 35386 MW; 29DD948706EB7143 CRC64;

Query Match 53.4%; Score 924.5; DB 1; Length 314;
Best Local Similarity 56.6%; Pred. No. 6,3e-76;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

1 MRAAAAAGGVRTAALL--LGLHMAAPARCEEDYDYGQAE--PLH-GRSYSKPPQCID 55
1 MGIGREGEGRGAALGVLLALGALLAVGASSEYDYVSFGSDIGPQSGFYTKPPQCYD 60

56 IPADPLPLCHTVGKRRRLPMLLEHESLAEPYKQASMLPLARCHSDTQVFLCSLPAPY 115
61 IPADPLPLCHTVGKRRRLPMLLEHESLAEPYKQASMLPLARCHSDTQVFLCSLPAPY 120

116 CLDRPIYPCRSGLCAEVRAGCAPLMEAYGFPMPMLCHKRPFLNDICIAVOFGH-IPATA 174
121 CLDRPIYPCRSGLCAEVRAGCAPLMEAYGFPMPMLCHKRPFLNDICIAVOFGH-IPATA 179

175 PAVTKIQAQCEMEHSADGLMEQSSDPFVYKRIKIKIENGDRKLIQAQKKKKLKPGE 234
180 PGTTVCPCPDNLTKEBAIEHLCASEFALRMKIKKEKKGNDKIV--PKKKKKPLKGP 237

235 LKRDYKRLYLHMKNGAGCPGPDLSLAGSFLYMGKRVGQQLLMAVYRDKKKNKMKRA 294
238 IKKKDKLKLVLTKNGADPCCHQLDNLSSHFLIMGRKVSQYLLTLAIHKKKDKKNKEKPF 297

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QY 295 VKEMESYPCSLYYPF 310
DB 298 MKMKNHCECPRQSVF 313

RESULT 10
SFRP1_BOVIN STANDARD; PRT; 308 AA.
AC 09116;
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE secreted frizzled-related protein 1 precursor (sFRP-1) (frizzled in
DE aorta protein) (FrzA protein).
GN Name=SFRP1; Synonyms=FRZA;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=ortic endothelium;
RX MEDLINE=99316255; PubMed=10381896;
RA Duplaa C., Jaepard B., Moreau C., D'Amore P.A.;
RT "Identification and cloning of a secreted protein related to the
RT cysteine-rich domain of frizzled: evidence for a role in endothelial
RT cell growth control.";
RL Circ. Res. 84:1433-1445(1999).

-1- FUNCTION: Soluble frizzled-related proteins (sFRPs) function as
modulators of Wnt signaling through direct interaction with Wnts.
They have a role in regulating cell growth and differentiation in
specific cell types. sFRP1 decreases intracellular beta-catenin
levels (By similarity). Has antiproliferative effects on vascular
cells, in vitro and in vivo, and can induce, in vivo, an
angiogenic response. In vascular cell cycle, delays the G1 phase
and entry into the S phase (By similarity). In kidney development,
inhibits tubule formation and bud growth in metanephroi (By
similarity). Inhibits WNT1/WNT4-mediated TGF-dependent
transcription.
-1- SUBUNIT: Interacts with WNT1, WNT2, WNT4 and WNT8 and FRZB6 (By
similarity).
-1- SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular
matrix-associated. Released by heparin-binding.
-1- TISSUE SPECIFICITY: Highest levels in aortic endothelium, heart,
spleen and eye. Lower levels in lung, brain and kidney. Weak
expression in liver, skeletal muscle and the medial layer of the
aorta. In the cortical brain, localized to neurons and small blood
vessels. In the retina, localized to the inner and outer nuclear
layers with high expression in the neuronal cell bodies. In the
heart, restricted to myocytes. In lung, highest expression found
in the epithelium of terminal bronchioles. In kidney, localized to
the epithelium of collecting ducts of the medulla and, in spleen,
expression restricted to the red pulp in cells associated with the
sinuses.
-1- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By
similarity).
-1- SIMILARITY: Belongs to the secreted frizzled-related protein
(sFRP) family.
-1- SIMILARITY: Contains 1 FZ (frizzled) domain.
-1- SIMILARITY: Contains 1 NTR domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL, U85945; AAB67062.1; -; mRNA.
DR HSSP, Q61091; 110Y.
DR InterPro, IPR000024; Fz_domain.

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DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PRO15759; NTR; 1.
 DR SMART; SM00643; G345C; 1.
 DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS00189; NTR; 1.
 DR Developmental protein; Differentiation; Glycoprotein; Signal;
 KM Wnt signaling pathway;
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 308 Secreted frizzled-related protein 1.
 FT DOMAIN 47 163 FZ.
 FT DOMAIN 180 300 NTR.
 FT CARBOHYD 167 167 N-linked (GlcNAc...) (by similarity).
 FT DISULFID 52 115 By similarity.
 FT DISULFID 62 108 By similarity.
 FT DISULFID 99 134 By similarity.
 FT DISULFID 123 160 By similarity.
 FT DISULFID 127 151 By similarity.
 FT DISULFID 180 250 By similarity.
 FT DISULFID 183 252 By similarity.
 FT DISULFID 197 300 By similarity.
 SQ SEQUENCE 308 AA; 34763 MW; 184D138B31123FEB CRC64;

Query Match 52.6%; Score 910.5; DB 1; Length 308;
 Best Local Similarity 57.1%; Pred. No. 1.2e-74;
 Matches 177; Conservative 48; Mismatches 72; Indels 13; Gaps 6;

QY 5 AAAGVRTAALALLGALHMAPRCEEDYDYGMAE---PLNGRSYKPPQCLIDIPADIP 61
 DB 7 AAAG-----ALTLAAGIL--AAGSASEDYVSFGSDIGAYQSGRFYTKPPQCVDPADIR 60
 QY 62 LCHTGYGKRMRLPNLLHESLAENVKQASWMLPLAKRCHSDTPQVFLCSLFPVCLDRPI 121
 DB 61 LCHNHYGKRMVLPNLLHETMAENVKQASWVPLLNKCHIGIQVFLCSLFPVCLDRPI 120
 QY 122 YPCRSICEAVRAGCAPLMEAYGFPWPPEMLHCHKFPLDNDLCIAVQFGH-LPATAPEPTKI 180
 DB 121 YPCRMICEAVRDSCEVWQFPFGYFPEMLKCKDFP-EGDVCIAMTPPNTTEASKPGSTTV 179
 QY 181 CAQCEMEHSADGLMEQCSSDPFVVKRIKEIKIENGDRKLGAQKKKLLKPGPLRKQDT 240
 DB 180 CPQCNELKSEAIIEHLKASEFALRMKRIKVEKKGNDKKIV--PKKKKPLKGPICKEL 237
 QY 241 KSLVLMKRGAGCCPQDLSLAGSFLVNGRKVDGQLLMAVTRMDKKNKEMKFAVYFMS 300
 DB 238 KKLVLTKRGAGDCPCHQDNLSHNPLIMGRKYSQYLTLAIHKMDKKNKEFTFMKMKM 297
 QY 301 YPCSLYYPF 310
 DB 298 HECPTQSVF 307

RESULT 11
 Q505A2_MOUSE PRELIMINARY; PRT; 314 AA.

AC Q505A2;
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DE 13-SEP-2005 (Tremblrel. 31, Last annotation update)
 DE Secreted frizzled-related sequence protein 1.
 GN Name=Strpl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange S.J.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schin J.B., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RG NIH MCC Project;
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC094662; AA094662.1; -; mRNA.
 SQ SEQUENCE 314 AA; 35412 MW; 3D98A15127DFA421 CRC64;

Query Match 52.5%; Score 909; DB 2; Length 314;
 Best Local Similarity 55.6%; Pred. No. 1.7e-74;
 Matches 174; Conservative 50; Mismatches 81; Indels 8; Gaps 5;

QY 2 RAAGAVRTAALALLGALHMAPRCEEDYDYGMAE---PLNGRSYKPPQCLIDIPADIP 58
 DB 5 RSARRGGAASGVLLAAL--LAAGSASEDYVSFGSDISYGSGRFYTKPPQCVDPADIR 63
 QY 59 DIPCHTGYGKRMRLPNLLHESLAENVKQASWMLPLAKRCHSDTPQVFLCSLFPVCLDRPI 118
 DB 64 DRLCHNHYGKRMVLPNLLHETMAENVKQASWVPLLNKCHMGTQVFLCSLFPVCLDRPI 123
 QY 119 RPIYCRSLICEAVRAGCAPLMEAYGFPWPPEMLHCHKFPLDNDLCIAVQFGH-LPATAPEPTKI 177
 DB 124 RPIYCRMLICEAVRDSCEVWQFPFGYFPEMLKCKDFP-EGDVCIAMTPPNTTEASKPG 182
 QY 178 TKICQCEMEHSADGLMEQCSSDPFVVKRIKEIKIENGDRKLGAQKKKLLKPGPLRKQDT 237
 DB 183 TTVCPQCNELKSEAIIEHLKASEFALRMKRIKVEKKGNDKKIV--PKKKKPLKGPICKEL 240
 QY 238 KOTKRLVLMKRGAGCCPQDLSLAGSFLVNGRKVDGQLLMAVTRMDKKNKEMKFAVYF 297
 DB 241 KELKRLVFLKRGAGDCPCHQDNLSHNPLIMGRKYSQYLTLAIHKMDKKNKEFTFMKMKM 300
 QY 298 MFSYPCSLYYPF 310
 DB 301 MNHSCPTQSVF 313

RESULT 12
 SFRPL_MOUSE STANDARD; PRT; 314 AA.

AC Q8C4U3; O08861; Q8R1J4;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Secreted frizzled-related protein 1 precursor (sfrp-1).
 GN Name=Strpl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (mRNA), AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic eye;
 RA MEDLINE=97250455; PubMed=9096311; DOI=10.1073/pnas.94.7.2859;

RA Ratner A., Hsieh J.-C., Smallwood P.M., Gilbert D.J., Copeland N.G.,
 RA Jenkins N.A., Nathans J.;
 RT "A family of secreted proteins contains homology to the cysteine-rich
 RT ligand-binding domain of frizzled receptors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kleener R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
 RA Diachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnell N.A., Peters G.J., Abramson R.D., Millhy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.T., Skalska U., Smalys D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 43-314.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354663; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oseko N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baldrelli R., Hill D.P., Bult C., Hune D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisai R.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guenrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Masushima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sempie C.A., Seton M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilm L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RN [4]
 RN FUNCTION AS AN ANGIOGENIC FACTOR.
 RP PubMed=15306229; DOI=10.1016/j.cardiores.2004.05.006;
 RA Ezan J., Leroux L., Barrandon L., Dufourcq P., Jaspard B., Moreau C.,
 RA Allieres C., Darot D., Couffignal T., Duplaa C.;
 RT "Fzra/sFRP-1, a secreted antagonist of the Wnt-Frizzled pathway,
 RT controls vascular cell proliferation in vitro and in vivo.";
 RT Cardiovasc. Res. 63:731-738(2004).
 RN [5]
 RN DEVELOPMENTAL STAGE.
 RP PubMed=9739103; DOI=10.1016/S0925-4773(98)00072-0;

RA Leinleiter C., Bach A., Geesler M.;
 RT "Developmental expression patterns of mouse sFRP genes encoding
 RT members of the secreted frizzled related protein family.";
 RT Mech. Dev. 75:29-42(1998).
 RN [6]
 RN INTERACTION WITH WNT9, AND DEVELOPMENTAL STAGE.
 RP PubMed=10640709; DOI=10.1016/S0925-4773(99)00236-1;
 RA Jaspard B., Couffignal T., Dufourcq P., Moreau C., Duplaa C.;
 RT "Expression pattern of mouse sFRP-1 and wnt-8 gene during heart
 RT morphogenesis.";
 RT Mech. Dev. 90:263-267(2000).
 CC -1- FUNCTION: Soluble frizzled-related proteins (sFRPs) function as
 CC modulators of Wnt signaling through direct interaction with Wnts.
 CC They have a role in regulating cell growth and differentiation in
 CC specific cell types. sFRP decreases intracellular beta-catenin
 CC levels (By similarity). Has antiproliferative effects on vascular
 CC cells, in vitro and in vivo, and can induce, in vivo, an
 CC angiogenic response. In vascular cell cycle, delays the G1 phase
 CC and entry into the S phase. In kidney development, inhibits tubule
 CC formation and bud growth in metanephros (By similarity). Inhibits
 CC WNT1/WNT4-mediated TGF-dependent transcription (By similarity).
 CC -1- SUBUNIT: Interacts with WNT1, WNT2, WNT4 and
 CC FRZB5 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular
 CC matrix-associated. Released by heparin-binding (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in kidney and embryonic
 CC heart. Also highly expressed in the eye, where it is principally
 CC localized to the ciliary body and the lens epithelium. Weaker
 CC expression in heart, lung and brain. In the brain, is expressed
 CC exclusively in the choroid plexus.
 CC -1- DEVELOPMENTAL STAGE: In the developing kidney expressed at 13.5
 CC dpc in the periphery of the metanephros and surrounding the uretic
 CC and nephrogenic tubules. At 14.5 dpc, expression decreases in the
 CC outer cortical cells and becomes visible in the tubular parts of
 CC the nephron. From 15.5 dpc, highly expressed in the future loops
 CC of Henle. In the developing CNS, expression located to the
 CC forebrain and hindbrain. At 8.0 dpc, expressed in the future
 CC forebrain and in the ventral portion of the presumptive hindbrain.
 CC At 8.5 dpc, expression is maintained in these tissues with a
 CC strong signal in rhombomere 4. Until 11.5 dpc, expression
 CC continues in the hindbrain with additional expression at 9.5 dpc
 CC and 10.5 dpc, in the nasal and ephranchial placodes. In the
 CC forebrain, initial expression is found in the preencephalon of the
 CC forebrain, and then strong expression in the telencephalic vesicle
 CC up to 15.5 dpc. Expression is then found in specific cell
 CC populations throughout the brain. In the developing eye,
 CC expression, by 10.5 dpc, is confined to ectodermal cells overlying
 CC the dorsal part of the optic cup. In later stages, expression
 CC limited to the lens fiber cells and the future pigmented retina.
 CC By 15.5 dpc, expression is confined to the anterior part of the
 CC lens. During limb development, barely expressed until later
 CC stages, when it is found in the distal part of the separating
 CC phalanges. In other developing structures, expressed in nasal
 CC placodes at 9.5 dpc, in medial nasal processes at E10.5 and then
 CC in the anterior portion of the invaginating olfactory epithelium.
 CC At 15.5 dpc, expressed on the basal side of the nasal epithelium.
 CC Also expressed in developing teeth, with the highest levels at
 CC 15.5 dpc and 16.5 dpc in the mesenchyme and the dental epithelium
 CC of the developing molars. As well, expressed in the ventral body
 CC wall, in the mesenchyme derived adrenal cortex, the cochlear
 CC epithelium and the branching epithelium of the salivary gland. In
 CC the developing heart, weakly expressed from 8.5 dpc to 12.5 dpc
 CC heart endocardium and myocardium. From 8.5 dpc to 12.5 dpc
 CC expressed in cardiomyocytes. At 9.5 dpc, expression found in the
 CC common ventricular and atrial chamber of the developing heart, in
 CC the aortic sac and in the sinus venosus. High expression found
 CC from 11.5 dpc-12.5 dpc, in the trabeculated wall of the
 CC ventricular chamber together with the wall of the atrial chamber.
 CC Expression also found in the muscular part of the interventricular
 CC septum. From 9.5 dpc-11.5 dpc expression in the visceral yolk sac
 CC confined to the inner lining endothelial cell layer. Expression
 CC in the developing heart decreases after 14.5 dpc.
 CC -1- DOMAIN: The F2 domain is involved in binding with Wnt ligands (By


```

CC similarity).
CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
CC (sfrp) family.
CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U88566; AAC53145.1; -; mRNA.
CC EMBL: BC024495; AAH24495.1; -; mRNA.
CC EMBL: AK081052; BAC38123.1; -; mRNA.
CC HSSP: OC1091; 11UY.
CC MGI: MGI:892014; Strp1.
CC GO: GO:0005615; C:extracellular space; TAS.
CC InterPro: IPR000024; Fz_domain.
CC InterPro: IPR001134; Netrin_C.
CC Pfam: PF01392; Fz; 1.
CC SMART: SMART:PF01759; NTR; 1.
CC SMART: SMART:SM00643; C345C; 1.
CC PROSITE: PS50038; FRI; 1.
CC PROSITE: PS50189; NTR; 1.
CC Developmental protein; Differentiation; Glycoprotein; Signal;
CC Wnt signaling pathway.
CC KMWnt signaling pathway.
CC FT SIGNAL 1 31 Potential.
CC FT CHAIN 32 314 Secreted frizzled-related protein 1.
CC FT DOMAIN 53 169 FZ.
CC FT CARBOHYD 173 173 N-linked (GlcNAc...) (By similarity).
CC FT DISULFID 58 121 By similarity.
CC FT DISULFID 68 114 By similarity.
CC FT DISULFID 105 140 By similarity.
CC FT DISULFID 129 166 By similarity.
CC FT DISULFID 133 157 By similarity.

Query Match 52.2%; Score 903; DB 1; Length 314;
Best Local Similarity 55.3%; Pred. No. 5; 9e-74; Mismatches 82; Indels 8; Gaps 5;
Matches 173; Conservative 50;

2 RAANAAGVYRTALALLGLAHWPACSEYDYVGMQAE---PLHGRSYKPPQCLDIPA 58
5 KSRKRGGAAGVLLALAAHL-LAAGSASRYDYVSFOSDGSYGSRFTTKPPQCDIVP 63
59 DLPLCHTVGYKRNRLPNLLEHESLAHYKQASWMLPLAKRCHSDTQVFLCSLFAVVCID 118
64 DLPLCHTVGYKRNRLPNLLEHESLAHYKQASWMLPLAKRCHSDTQVFLCSLFAVVCID 123
119 RPIYPCRSLSCEAVRAGCAPLMEAYGPPWPMELCHKFPPLNDICIAVQFQH-LPATAFPV 177
124 RPIYPCRSLSCEAVRAGCAPLMEAYGPPWPMELCHKFPPLNDICIAVQFQH-LPATAFPV 182
178 TKICACCEMHSADGLMEQCSSDFVYVYKRIKEIKIENGGRKULIGAOKKKKLLKPPPLR 237
183 TKICACCEMHSADGLMEQCSSDFVYVYKRIKEIKIENGGRKULIGAOKKKKLLKPPPLR 240
238 KDTKRLVLLHMKNGAGCPQOLDISLAGSFLVMGRKVDQQLLMAVYRMDKKKEMKFAVYK 297
241 KELKALVLLFKNGADGCPHQDLNLSHNFILMGRKVSQYLLTAIHMKWDKKKKEFKPMKR 300
298 MESYPCSLYYPFF 310
301 MKNHCEPTFQSVF 313

```

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Secreted frizzled-related protein 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_Taxid=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15210177; DOI=10.1016/j.mod.2004.03.003;
RA Esteve P., Lopez-Rios J., Bovolenta P.,
RT "SFRP1 is required for the proper establishment of the eye field in
RT the medaka fish."
RL Mech. Dev. 121:687-701(2004).
DR EMBL: AY560904; AAS59408.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; P:transmembrane receptor activity; IEA.
DR GO: GO:0007275; P:development; IEA.
DR GO: GO:0016055; P:wnt receptor signaling pathway; IEA.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SMART:PF01759; NTR; 1.
DR SMART: SMART:SM00643; C345C; 1.
DR PROSITE: PS50038; FRI; 1.
DR PROSITE: PS50189; NTR; 1.
DR SEQUENCE 306 AA; 34955 MW; 6D49B0FB9682C48C CRC64;

Query Match 49.2%; Score 851; DB 2; Length 306;
Best Local Similarity 52.7%; Pred. No. 3; 2e-69; Mismatches 74; Indels 26; Gaps 7;
Matches 164; Conservative 47;

11 RTAALALLGLAHWPACSEYDYVGMQAEPLH-GRSYKPPQCLDIPAFLCHTVGYK 69
10 RWTQVLLAATVTCGA---SEYE-YTMAAGSYNGRGYGAQPCVDIDPDLPLCHTVGYT 64
70 RKRRLPNLLEHESLAHYKQASWMLPLAKRCHSDTQVFLCSLFAVVCIDRPIYPCRSICE 129
65 QMLPLLEHETMAAVKQASWMLPLHKNCHDKDTQVFLCALFAVCEHPPIYPCRWLCE 124
130 AVRAGCAPLMEAYGPPWPMELCHKFPPLNDICIAV-----QFGLPATAFPVYK 179
125 TYRDCSPFLMEAFGPPWPMELTCDKFPDG-VCIATVQPMATEATPSSHSA----- 176
180 ICAQCEMHSADGLMEQCSSDFVYVYKRIKEIKIENGGRKULIGAOKKKKLLKPPPLR 239
177 -CPDCNEIKNDAMLENICASBFAKAKIKEYKQENMDRKVI-LQRRKRMVQGNLKKRD 234
240 TKRVLVLLHMKNGAGCPQOLDISLAGSFLVMGRKVDQQLLMAVYRMDKKKEMKFAVYK 299
235 LKKLFLVLLHMKNGAGCPQOLDLENQYLIMGRKVDKQPLTGIHMKWDKKKKEFKKIMK 294
300 SYPCSLYYPFF 310
295 NYKCPAFENVF 305

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RESULT 13
Q6GZK1 ORYLA PRELIMINARY; PRT; 306 AA.
AC Q6GZK1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

RESULT 14
SFRP1 CHICK STANDARD; PRT; 314 AA.
AC Q9DBQ1;
DT 10-MAY-2005 (rel. 47, Created)
DT 10-MAY-2005 (rel. 47, Last sequence update)
DT 10-MAY-2005 (rel. 47, Last annotation update)
DE Secreted frizzled-related protein 1 precursor (sfrp-1) (Csfrp1).
GN Name=SFRP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.

OX NCBI_TaxId=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND DEVELOPMENTAL STAGE.
 RX MEDLINE=20480381; PubMed=11025229; DOI=10.1016/S0925-4773(00)00421-4;
 RA Esteve P., Morcillo J., Boyolenta P.;
 RT "Early and dynamic expression of cSfrp1 during chick embryo development.";
 RL Mech. Dev. 97:217-221(2000).
 CC -1- FUNCTION: Soluble frizzled-related proteins (sFRPs) function as modulators of Wnt signaling through direct interaction with Wnts. They have a role in regulating cell growth and differentiation in specific cell types.
 CC -1- SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular matrix-associated. Released by heparin-binding (By similarity).
 CC -1- DEVELOPMENTAL STAGE: Expression first detected at the pre-streak stage, uniformly distributed throughout the blastula. During primitive streak formation, expression localized to the anterior blastoderm including the anterior tip of primitive streak. At the beginning of Hensen's node regression, strongly expressed, anterior to the node, in the ectoderm, in the presumptive neuroectoderm as well as in prechordal and lateral mesoderm. Later expression in the blastoderm anterior to Hensen's node. During neurulation, high levels detected in the anterior neural plate. Expression also found in the neural folds including the pre-migratory cephalic neural crest cells, in the anterior ectoderm, in the lateral mesoderm, in the prechordal plate and weaker expression in the notochord. From stage 10-14, strong expression in the anterior neural tube, including the optic vesicles, where expression is limited to the presumptive neural retina and the overlying ectoderm. Later expression in the lens placode and the outer layer of the optic cup. Expression also in the prechordal plate, the Rathke's pouch and later in the infundibular region. Expression in head mesenchyme, including migrating cephalic neural crest cells. Restricted expression within the metencephalic vesicle and ventral neural tube. Also expressed in the notochord, the otic vesicles, dorsal mesocardium and the area vasculosa. From stages 18-26, expression found in the telencephalic vesicles, in the epiphysis, in the optic cup, the trigeminal ganglia, and in a band which occupies the basal plate of prosomere one. During neural tube differentiation, expression follows a rostro-caudal gradient. Expression appears in the floor plate and in cells that occupy the medial neural tube. Expression also localized to the mesenchyme of the developing branchial arches, the most distal and ventral portion of the developing limb buds, including the ectodermal apical ridge and to the mesoderm of the developing kidney.
 CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (by similarity).
 CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein (sFRP) family.
 CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL: AJ404652; CAC15041.1; -; mRNA.
 CC HSSP: P97401; IIUX.
 CC DR Ensembl: ENSGALG0000003473; Gallus gallus.
 CC DR InterPro: IPR000024; Fz domain.
 CC DR InterPro: IPR001134; Netrin_C.
 CC DR Pfam: PF01392; Fz; 1.
 CC DR Pfam: PF01759; NTR; 1.
 CC DR SMART: SM00643; C345C; 1.
 CC DR SMART: SM00643; FRI; 1.
 CC DR PROSITE: PS50038; FZ; 1.
 CC DR PROSITE: PS50189; NTR; 1.
 CC DR Developmental protein; Differentiation; Glycoprotein; Signal; Wnt signaling pathway.
 KM Wnt signaling pathway.
 FT SIGNAL 1 Potential.

FT CHAIN 32 314 Secreted frizzled-related protein 1.
 FT DOMAIN 53 169 FZ.
 FT FT 186 306 NTR.
 FT FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
 FT FT DISULFID 58 121 By similarity.
 FT FT DISULFID 68 114 By similarity.
 FT FT DISULFID 105 114 By similarity.
 FT FT DISULFID 129 140 By similarity.
 FT FT DISULFID 133 157 By similarity.
 FT FT DISULFID 133 157 By similarity.
 FT FT DISULFID 189 258 By similarity.
 FT FT DISULFID 203 306 By similarity.
 SQ SEQUENCE 314 AA; 35280 MM; A7AE6F9F6F5D33C CRC64;
 Query Match 48.4%; Score 838; DB 1; Length 314;
 Best Local Similarity 54.6%; Pred. No. 5,1e-68;
 Matches 166; Conservative 48; Mismatches 78; Indels 12; Gaps 7;
 QY 1 MRAAAGGVRPALALL--LGALHMAPRCSEHYTGQAE--PL-HGRSYSKPPQCLD 55
 DB 1 MGVRSEGGRRGALGVLLAGVALLAVGASSEYDVYSQDLGFPQGRFETKPHQCV 60
 QY 56 IPADPLCHGVGKRMRLPNLLEHESLAENVQQAASMTPLAKRCHSPDTQVFLCSLP 115
 DB 61 IPADRLCHSVGDKMVLPNLLEHETMBVKHQAASSWPLANKCHMGTQVFLCSLP 120
 QY 116 CUDRIYPCRSICEAVRAGCAPLMEAYGPPMEMLCHKFPDLNDLCIAVOFGH-LPATA 174
 DB 121 CUDRIYPCRSICEAVRAGCAPLMEAYGPPMEMLCHKFPDLNDLCIAVOFGH-LPATA 179
 QY 175 PPTVYKICQACEMESADGLMEQCSDFVVKRIKEIKIENGDRKLTGAKKKLLKGP 234
 DB 180 PGTIVYCPCCDNEMSESAIVETLCSEFALNKTITVEVKENGDKYII--PRKRALKGP 237
 QY 235 LKRKDTKRLVLMKRGAGCPQPDLSLGSFLVMGRKVDGOLLMAVYRMDKKNKEMFA 294
 DB 238 LKRRKDTKRLVLMKRGAGCPQPDLSLGSFLVMGRKVDGOLLMAVYRMDKKNKEMFA 295
 QY 295 VKFM 298
 DB 296 -KFM 298
 DB
 RESULT 15
 ID Q9Y124 XENLA PRELIMINARY; PRT; 311 AA.
 AC Q9Y124;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Frizzled-related protein.
 GN Name:frzA;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Xu Q., D'Amore P., Sokol S.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF049908; AAD02492.1; -; mRNA.
 DR HSSP: O61091; IIUY.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; P:transmembrane receptor activity; IEA.
 DR GO: GO:0007275; P:development; IEA.
 DR GO: GO:0016055; P:Wnt receptor signaling pathway; IEA.
 DR InterPro: IPR000024; Fz domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00643; C345C; 1.
 DR SMART: SM00643; FRI; 1.

DR PROSITE; PSS0038; FZ; 1.
DR PROSITE; PSS0189; NTR; 1.
SQ SEQUENCE 311 AA; 35718 MW; 81C9E7153F445401 CRC64;

Query Match 48.4%; Score 836.5; DB 2; Length 311;
Best Local Similarity 55.1%; Pred. No. 7e-68;
Matches 158; Conservative 46; Mismatches 66; Indels 17; Gaps 7;

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QY 20 GALHMAPACEEYDYWGQ---AEPLHGRSYSGPPQCDIPADLPLCHTVGKRMRLPN 75
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18 GILSQVP-QASEYDVVSFQPDLAGRYQSGRFTSRPAQCLEIPQDMTLCHGVGNKRVLPN 76
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 76 LLEHESIAEVKQOASSWMLPLAKRCHSDTQVFLCSLFAPVCLDRPIYPCKSLCEAVRAGC 135
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 77 LLDSEETMAEVKYQASSWVPLSKKCHPSYQVFLCSLFAPLCLDRPYPCRLCESYRDAC 136
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 136 APLMEAYGFPWPEMLHCHKRPLDNDLCIAVQFGHLP-ATAFP--VTKIQAQCEMEHSAD 191
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 EPMQYFGFHWPEMLRCEQYPTEDVCIAV--HLPNATOAPRSRKTEVCPQCDSEIKAD 193
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 192 GMEQWCSSDFVYKMRIRKIKIENGDRKLIQAQKKKLLKPGPLKRDTRRLVLAHKNGA 251
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 SLYEHWCASDFALKVSIREVRENKGRKLL--LRKSKALKGPIQKQDMABLVLTKNGA 251
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 252 GCPCPQLDSLAGSFLVMGRKVDGQLLMAVYRWDKKEMKFAVKFM 298
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 NCPCHQLDQLKGQFLVLSPPAKAKQHLLTAIHKWDKTNREFN---RFM 295
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: March 22, 2006, 22:42:16
Job time : 234 secs

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Query Match	16.1%;	Score 279;	DB 7;	Length 325;
Best Local Similarity	26.1%;	Pred. No. 1.9e-20;		
Matches	85;	Conservative	51;	Mismatches 106;
			Indels	84;
			Gaps	13;

RESULT 5

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-281-36

Query Match      16.1%; Score 278; DB 7; Length 591;
Best Local Similarity 36.7%; Pred. No. 4.9e-20;
Matches 65; Conservative 23; Mismatches 53; Indels 36; Gaps 7;

OY   AACGVRFAALALLLGLAHMAPARCEEDYVGQMAEPRLHGSSYSKPPQCLDIPADLPICHT 65
Db    AAGCA-----ALEIG-----RFDPERGRG-AAPCQAVRI-----PWCRCG 49

OY   VGYGRMELPNULHEHSIAEYKQAASSWLPLAKRCHSDTQVFLCSLPAPVCIDR---PIY 122
Db    VGYGRMELPNULHGTSGSAAAEIABEFAPLVQYGCHSHLRFLCSLVAAPMCTDVSTPIP 109
     50 IGVNLTMPNLHGTSGSAAAEIABEFAPLVQYGCHSHLRFLCSLVAAPMCTDVSTPIP 109

OY   PCSRLCEAVAGCAPLMEAYGFPMPEMLHCKRPDLND--LCIAVOFGHLPATAPP 176
Db    ACSRMCCQALRCAPIMEQFNFGMPDSLDCAQLPTRNDPHALCWEADEN--ATAGP 163

RESULT 10
US-11-054-281-128
; Sequence 128, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/11/054,281
; PRIOR FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 128
LENGTH: 591
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-281-128

Query Match      16.1%; Score 278; DB 7; Length 591;
Best Local Similarity 36.7%; Pred. No. 4.9e-20;
Matches 65; Conservative 23; Mismatches 53; Indels 36; Gaps 7;

```

Publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS THEREOF FOR DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1306
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-720-1306

Query Match 23.7%; Score 410.5; DB 7; Length 180;
Best Local Similarity 50.9%; Pred. No. 5e-34;
Matches 84; Conservative 21; Mismatches 49; Indels 11; Gaps 4;

QY 14 ALALLGALHMAPARCEVDYVGMQABPLHGRSXSXKPPQCDIPADLPLCHTVGKEMRL 73
DB 7 SLILLFLASHCCLGASAGLPLFG-QDPDSYKRSNCKP-----IFANILQCHGIEYQNRLL 60
QY 74 PNLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAVC---LDRPIYPCRSICEA 130
DB 61 PNLLGHETKEVLEQAQAWIPLVVKQCHPDTKFKFLCSLFAVCDDIDETIQCHSLCVQ 120
QY 131 VRAGCAPLMEAYGFPPEMHLCHKFPDNDLCIAVQGH--LPRIT 173
DB 121 VKORCAPVMSAGFPGPMDMLECDRFPQDNDLCIPLASSDHLIPAT 165

RESULT 6
US-11-054-281-306
Sequence 306, Application US/11054281
GENERAL INFORMATION:
APPLICANT: Mezes et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-240CIP
CURRENT APPLICATION NUMBER: US/11/054,281
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: 60/261,014
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/318,410
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 10/044,564
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 306
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: sequence
US-11-054-281-306

Query Match 18.3%; Score 316.5; DB 7; Length 117;
Best Local Similarity 51.8%; Pred. No. 9e-25;
Matches 57; Conservative 14; Mismatches 36; Indels 3; Gaps 1;

QY 57 PADLPLCHTVGKEMRLPNLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAVC 116
DB 4 PILLPLCKDLGYNTSPNLLGHTTOEAGLELSQFPLNVAQCSPDILFFLCISYAVVC 63
QY 117 ---LDRPIYPCRSICEAVRAGCAPLMEAYGFPPEMHLCHKFPDNDLCI 163
DB 64 TADLPEILLPCRSICEAAREGCEPLMEKFGWPEFLRCDFPQVQNELCM 113

RESULT 7
US-11-184-005-7
Sequence 7, Application US/11184005
Publication No. US20050256052A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Malcolm JR.
APPLICANT: Hoang, Bang
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: METHOD OF MODULATING TISSUE
FILE REFERENCE: NIH133.1CFC3
CURRENT APPLICATION NUMBER: US/11/184,005
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 10/028051
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 08/822333
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 319
TYPE: PRT
ORGANISM: Xenopus laevis
US-11-184-005-7

Query Match 16.5%; Score 285; DB 7; Length 319;
Best Local Similarity 27.8%; Pred. No. 4.5e-21;
Matches 76; Conservative 50; Mismatches 93; Indels 54; Gaps 11;

QY 57 PADLPLCHTVGKEMRLPNLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAVC 116
DB 33 PVRLPMCKSMWNMTKMFNHLHSTOANALIBQFBLITTBESQDILFLCAMYABIC 92
QY 117 L-----DRPIYPCRSICEAVRAGCAPLMEAYGFPPEMHLCHKFPDNDLCIAVQF---- 167
DB 93 TIDFQHEPIKPKCSYCEARAGCEPILIKYHTTPESLACELEPYDRGVCISPEAYTV 152
QY 168 -----GHLPATAPPVTKICACQCEMEHSADGLMEQMCSSDFVYKRIKEI 211
DB 153 EGGTDSMPDFPMDNNGCGSTA---GEHCCKPMKASOKTYLKN--NYNVIVIRAKVEV 207
QY 212 KIENGDRKLIGAOKKKLLKPKPLK-RKDYRLVLHMKNGAGCCPPQDLSLAGSLVNGR 270
DB 208 KVKCHDATAI--VVEKEIKSLVINIPDVTLY----TNSGCLCPQLVA-NBEYITMGY 260
QY 271 K-----VDGQL-----LMAVYRWKK 287
DB 261 EDKERTLLVSGSLAEKMRDLAKKVRMDOK 293

RESULT 8
US-11-184-005-2
Sequence 2, Application US/11184005
Publication No. US20050256052A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Malcolm JR.
APPLICANT: Hoang, Bang
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: METHOD OF MODULATING TISSUE
FILE REFERENCE: GROWTH USING FRZB PROTEIN

Db 395 NFWKMKNNHECPTQSVF 412

RESULT 2
US-11-067-121-11

Sequence 2, Application US/11067121
Publication No. US20050261185A1
GENERAL INFORMATION:
APPLICANT: Martijn, Cecile
TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
PRIOR FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 295
TYPE: PRT
ORGANISM: Mus musculus
US-11-067-121-2

Query Match 35.9%; Score 620.5; DB 7; Length 295;
Best Local Similarity 44.1%; Pred. No. 6e-55;
Matches 127; Conservative 51; Mismatches 93; Indels 17; Gaps 7;

QY 13 ALALLLGLAHMAPARCEBYDYGWQAEPLHGRSYKSPPOCLDIPADLPICHTVGYKRRK 72
DB 6 ASLLLVLAASHCCLSARGFLFG--OPDFSXKRSNCKP-----IPANLQICHGIEYQNNR 59
QY 73 LNLLEHESLAIEYKQOASWMLPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLSCE 129
DB 60 LNLGHEHETKVEYLBQAGMIPVMKQCHPDTKFLCSLPAPVCDDDDDETIOPCHSLSV 119
QY 130 AVRAGCAPLMEAYGFPWPMELHCHKFPDLNDLCIAVOFGH--LPAT--APPVTKICAQCE 185
DB 120 QVKDCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLIPATEAP---KVCEACK 176
QY 186 MEHSADG-LMEQMCSSDFVVKRIKIKIENGDRKLIQAQKKKLLKPGPLKROTRLV 244
DB 177 TKNEDNDIMETLCKNDPALKIKVEKITIYNRDTKILLETKSKTIYKLVNGVSEBDLKSV 236
QY 245 LHMKGAGCPCPOLDSLGLSFLVMGRKVDGQLLMAVYRMDKKNKEMK 292
DB 237 WLKDSLOCTCEBNDINAPVLMGOKOGELVITSVKRMQKQREPK 284

RESULT 3
US-11-067-121-11

Sequence 11, Application US/11067121
Publication No. US20050261185A1
GENERAL INFORMATION:
APPLICANT: Martijn, Cecile
TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
PRIOR FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens

US-11-067-121-11

Query Match 35.5%; Score 614.5; DB 7; Length 295;
Best Local Similarity 43.9%; Pred. No. 2.4e-54;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 14 ALALLLGLAHMAPARCEBYDYGWQAEPLHGRSYKSPPOCLDIPADLPICHTVGYKRRK 73
DB 7 SLILLFLASHCCLSARGFLFG--OPDFSXKRSNCKP-----IPANLQICHGIEYQNNR 60
QY 74 LNLLEHESLAIEYKQOASWMLPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLSCE 130
DB 61 LNLGHEHETKVEYLBQAGMIPVMKQCHPDTKFLCSLPAPVCDDDDDETIOPCHSLSV 120
QY 131 VRAGCAPLMEAYGFPWPMELHCHKFPDLNDLCIAVOFGH--LPAT--APPVTKICAQCE 186
DB 121 VKDCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLIPATEAP---KVCEACK 177
QY 187 MEHSADG-LMEQMCSSDFVVKRIKIKIENGDRKLIQAQKKKLLKPGPLKROTRLV 245
DB 178 KNDNDNDIMETLCKNDPALKIKVEKITIYNRDTKILLETKSKTIYKLVNGVSEBDLKSV 237
QY 246 HMKNGAGCPCPOLDSLGLSFLVMGRKVDGQLLMAVYRMDKKNKEMK 292
DB 238 WLKDSLOCTCEBNDINAPVLMGOKOGELVITSVKRMQKQREPK 284

RESULT 4

US-11-051-720-1701
Sequence 1701, Application US/11051720
Publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHO
FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
PRIOR FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1701
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-720-1701

Query Match 35.5%; Score 614.5; DB 7; Length 295;
Best Local Similarity 43.9%; Pred. No. 2.4e-54;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 14 ALALLLGLAHMAPARCEBYDYGWQAEPLHGRSYKSPPOCLDIPADLPICHTVGYKRRK 73
DB 7 SLILLFLASHCCLSARGFLFG--OPDFSXKRSNCKP-----IPANLQICHGIEYQNNR 60
QY 74 LNLLEHESLAIEYKQOASWMLPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLSCE 130
DB 61 LNLGHEHETKVEYLBQAGMIPVMKQCHPDTKFLCSLPAPVCDDDDDETIOPCHSLSV 120
QY 131 VRAGCAPLMEAYGFPWPMELHCHKFPDLNDLCIAVOFGH--LPAT--APPVTKICAQCE 186
DB 121 VKDCAPVMSAFGFPWPMLECDRFPQDNDLCIPLASSDHLIPATEAP---KVCEACK 177
QY 187 MEHSADG-LMEQMCSSDFVVKRIKIKIENGDRKLIQAQKKKLLKPGPLKROTRLV 245
DB 178 KNDNDNDIMETLCKNDPALKIKVEKITIYNRDTKILLETKSKTIYKLVNGVSEBDLKSV 237
QY 246 HMKNGAGCPCPOLDSLGLSFLVMGRKVDGQLLMAVYRMDKKNKEMK 292
DB 238 WLKDSLOCTCEBNDINAPVLMGOKOGELVITSVKRMQKQREPK 284

RESULT 5

US-11-051-720-1306
Sequence 1306, Application US/11051720

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 22:44:07 ; Search time 23 Seconds

(without alignments)
394.498 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730

Sequence: 1 MRAAAAGVXTALALLG.....MSYPCSLYPPFGAEPH 317

Scoring table:

BLOSUM62
Gap0 10.0, Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata1/pubpaa/US08_NEM_PUB.pep.*
2: /cgn2_6/ptodata1/pubpaa/US06_NEM_PUB.pep.*
3: /cgn2_6/ptodata1/pubpaa/US07_NEM_PUB.pep.*
4: /cgn2_6/ptodata1/pubpaa/US09_NEM_PUB.pep.*
5: /cgn2_6/ptodata1/pubpaa/US10_NEM_PUB.pep.*
6: /cgn2_6/ptodata1/pubpaa/US11_NEM_PUB.pep.*
7: /cgn2_6/ptodata1/pubpaa/US12_NEM_PUB.pep.*
8: /cgn2_6/ptodata1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	916	52.9	413	6	US-10-821-234-989
2	620.5	35.9	295	7	US-11-067-121-2
3	614.5	35.5	295	7	US-11-067-121-11
4	614.5	35.5	295	7	US-11-051-720-1701
5	410.5	23.7	180	7	US-11-051-720-1306
6	316.5	18.3	117	7	US-11-054-281-306
7	285	16.5	319	7	US-11-184-005-7
8	279	16.1	325	7	US-11-184-005-2
9	278	16.1	591	7	US-11-054-281-36
10	278	16.1	591	7	US-11-054-281-128
11	278	16.1	592	7	US-11-054-281-127
12	277.5	16.0	585	7	US-11-054-281-92
13	276.5	16.0	319	7	US-11-184-005-8
14	275	15.9	325	7	US-11-184-005-4
15	273	15.8	585	7	US-11-127-877-63
16	270	15.6	592	7	US-11-054-281-126
17	269.5	15.6	586	7	US-11-054-281-93
18	268	15.5	581	7	US-11-067-231-153
19	268	15.5	581	7	US-11-054-281-22
20	268	15.5	581	7	US-11-054-281-91
21	267.5	15.5	549	7	US-11-054-281-129
22	265	15.3	530	7	US-11-054-281-94
23	253.5	14.7	537	7	US-11-152-366-43
24	253.5	14.7	537	7	US-11-169-041-132
25	253.5	14.7	537	7	US-11-169-041-134

26	252.5	14.6	111	7	US-11-184-005-6	Sequence 6, Appl
27	251.5	14.5	577	7	US-11-054-281-130	Sequence 130, App
28	251	14.5	580	7	US-11-054-281-95	Sequence 95, Appl
29	249.5	14.4	188	7	US-11-152-366-249	Sequence 249, Appl
30	243.5	14.1	111	7	US-11-184-005-5	Sequence 5, Appl
31	215	12.4	351	7	US-11-054-281-100	Sequence 100, Appl
32	211	12.2	346	7	US-11-054-281-97	Sequence 97, Appl
33	210.5	12.2	348	7	US-11-054-281-99	Sequence 99, Appl
34	209.5	12.1	348	7	US-11-054-281-69	Sequence 69, Appl
35	209.5	12.1	348	7	US-11-054-281-98	Sequence 98, Appl
36	207	12.0	346	7	US-11-186-284-189	Sequence 189, App
37	207	12.0	346	7	US-11-054-281-24	Sequence 24, Appl
38	207	12.0	346	7	US-11-054-281-96	Sequence 96, Appl
39	161	9.3	1113	7	US-11-067-811-4	Sequence 4, Appl
40	156	9.0	1042	7	US-11-152-366-283	Sequence 283, App
41	130	7.5	116	7	US-11-152-366-44	Sequence 44, Appl
42	130	7.5	433	7	US-11-137-465-47	Sequence 47, Appl
43	100.5	5.8	462	7	US-11-072-512-2086	Sequence 2086, Ap
44	88	5.1	488	7	US-11-169-041-176	Sequence 176, App
45	88	5.1	488	7	US-11-169-041-176	Sequence 176, App

ALIGNMENTS

RESULT 1	
US-10-821-234-989	
Sequence 989, Application US/10821234	
Publication No. US2005025511A1	
GENERAL INFORMATION:	
APPLICANT: Labat, Ivan	
APPLICANT: Stache-Grain, Birgit	
APPLICANT: Andermani, Susan	
APPLICANT: Tang, Y. Tom	
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia	
FILE REFERENCE: 821A	
CURRENT APPLICATION NUMBER: US/10/821,234	
CURRENT FILING DATE: 2004-04-07	
PRIOR APPLICATION NUMBER: US 60/462,047	
PRIOR FILING DATE: 2003-04-07	
NUMBER OF SEQ ID NOS: 1704	
SOFTWARE: PC_SEQ_genes Version 1.0	
SEQ ID NO 989	
LENGTH: 413	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-821-234-989	
Query Match	52.9%; Score 916; DB 6; Length 413;
Beat Local Similarity	56.3%; Pred. No. 1.4e-84;
Matches 179; Conservative	50; Mismatches 77; Indels 12; Gaps 7;
QY	2 RAAAAAG---GRTAALL--LGLHWAAPARCEBYDYGQAE--PLH-GRSYKPPQC 53
DB	98 RAGMGIGSEGGRGALGVLLALGALLAVASASEYDVVSQSDIGYQSGRFTYKPPQC 157
QY	54 LDIPADLEPLCTTVGKRRRLNLLHESLAVKQOASSWPLLARCSDTQVFLCSLFA 113
DB	158 VDIADLEPLCHNVGKKKVVLLNLEHETMAVVKQOASSWVPLNKGCHAGTQVFLCSLFA 217
QY	114 PVCLDRPIYPRSCAEAVRACAPLMEAYGPPWPMILCHKEPPLNDICIAVQFH-LPA 172
DB	218 PVCLDRPIYPRMICEAVRDSCEPVMQFFGFWPMLKCDXP-EGDVCIATTPPNATEA 276
QY	173 TAPVTKIACOCENHSHADGLMEQWSSDFVVKRIKIKITENGDRKLIGAOKKKLLKP 232
DB	217 SKPGTTVCPCPDNLSKSEALIEHLICASEFLRMKIKKVKKENGDKIV--PKKKKPKL 334
QY	233 GPLKAKDTKRLVLMKKGAGCPCLDLSLAGSFLVMGRKVDGQLLMAVYMDKKKEMK 292
DB	335 GPIKKKDKLKLVLVILKNGADCPCHQDLNLSHHFLIMGRKVSQYLLTAIHMKDKKKEFK 394
QY	293 FAVKFMFSYPCSLYPPF 310

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PRIORITY APPLICATION NUMBER: 60/261,029
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 10/044,564
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 585
TYPE: PRT
ORGANISM: Gallus gallus
US-11-054-281-92

Query Match      16.0%; Score 277.5; DB 7; Length 585;
Best Local Similarity 36.5%; Pred. No. 5.4e-20;
Matches 61; Conservative 22; Mismatches 57; Indels 27; Gaps 5;

OY      6 AAGGTRTAALLLGGALHMAPRCEEDVYGQMAEPLHGSR---XSPQCGLDIPADLP.L 62
DB      4 AAGLVRAVAL-----C-----WLHEHCAGLISSIDIERGDGRCPTEIFM 45
OY      63 CHTVGYKRMRLPNLLHEHSIAEVKOQASWMLPLAKRCHSDTOVFCLSFAPVCIDR--- 119
DB      46 CKDIGMYMTNRPNLMGHENQREAAIQIHERFAPLYBYGCHGLKPFCLSLYAPMCTEQYST 105
OY      120 PIYCRSICEAVRAGCAPMEAYGFPPPEMIHCHKFPILDND---LCI 163
DB      106 PIACRVWCSEQARLKCSPIMEQFNFKWPDSIDCSKLPIKNDPNYLICM 152

RESULT 13
US-11-184-005-8
Sequence 8, Application US/11184005
Publication No. US20050256052A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Malcolm JR.
APPLICANT: Hoang, Bang
TITLE OF INVENTION: METHOD OF MODULATING TISSUE
TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
FILE REFERENCE: NIH13.1CPC3
CURRENT APPLICATION NUMBER: US/11/184,005
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 10/028051
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 08/822333
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 319
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-11-184-005-8

Query Match      16.0%; Score 276.5; DB 7; Length 319;
Best Local Similarity 25.8%; Pred. No. 3.3e-20;
Matches 84; Conservative 52; Mismatches 106; Indels 83; Gaps 13;

OY      7 AGGRTATALL--GALHMARPCEEVDYWGQAEPHIGSYSKKPQCGLDIPADLP.CH 64
DB      12 AGLALAALCLRVRGA---RAACE-----PRITPLCK 42
OY      65 TVGYKRMRLPNLLHEHSIAEVKOQASWMLPLAKRCHSDTOVFCLSLFAPVCL---DRP 120
DB      43 SLPMNTMPRHLSHTQNNAILAEQPEGILGTHCSFDLLPFLCANVAPICTIDFGHEP 102

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GenCore version 5.1.7
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OM protein - nucleic search, us-10-768-566-1

Run on: March 23, 2006, 06:52:56 ; Search time 5745 Seconds
(without alignments)
3136.532 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAAGCVRATATALLG.....MFSYCSLYPFYGAABPH 317

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/absb/ABSSWEB.spool/US10768566/runat_22032006_155807_25230/app.query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss808
-USER=US10768566 @CCN 1 1 4939 @runat_22032006_155807_25230 -NCPUs=6 -ICPU=3
-NO_MAP -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pr:*
9: gb_ro:*
10: gb_srs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1730	100.0	1852	8	BC050435 Homo sapi
2	1730	100.0	1984	6	BD217902 Gene fam1
3	1730	100.0	1984	6	AX565716 Sequence

4	1730	100.0	1984	6	AX597116	Sequence
5	1730	100.0	1854	6	AX701369	Sequence
6	1730	100.0	1984	6	AF017988	Homo sapi
7	1730	100.0	1993	8	AF117758	Homo sapi
8	1730	100.0	1993	8	C0720585	Sequence
9	1682	97.8	1280	6	BA4023	Novel human
10	1656	95.7	1728	4	AF117757	Bos taurus
11	1617	93.5	1813	9	BC032921	Mus muscu
12	1613	93.2	1186	9	AF117759	Mus muscu
13	1613	93.2	210585	9	AC106128	Rattus no
14	1162.5	67.2	163348	9	AC119236	Mus muscu
15	1162.5	67.2	189196	9	ALC03804	Mouse DNA
16	1160.5	67.1	1946	5	BC074661	Xenopus t
17	1157.5	66.9	3043	5	AY164461	Xenopus 1
18	1155.5	66.9	3043	5	BC082632	Xenopus 1
19	1106.5	64.0	146124	8	AL358938	Human DNA
20	1089	62.9	1846	5	AY050560	Danio rer
21	1089	62.9	2006	5	BC085455	Danio rer
22	1077	62.3	265464	14	AC157384	Bos taurus
23	977	56.5	1755	6	CS105981	Sequence
24	924.5	53.4	945	11	AY891055	Synthetic
25	924.5	53.4	945	11	BT019677	Synthetic
26	924.5	53.4	1308	6	BD217906	Gene fam1
27	924.5	53.4	2078	6	AR253205	Sequence
28	924.5	53.4	2094	8	AF017987	Homo sapi
29	924.5	53.4	2602	6	AX099741	Sequence
30	924.5	53.4	4482	8	BC036503	Homo sapi
31	924.5	53.4	4500	6	AR253209	Sequence
32	917	53.0	942	6	AR361925	Sequence
33	917	53.0	942	6	AX482568	Sequence
34	916	53.0	1017	6	AR361926	Sequence
35	916	52.9	2075	6	AR253206	Sequence
36	916	52.9	2075	6	AR361924	Sequence
37	916	52.9	2075	6	AR433000	Sequence
38	916	52.9	2075	6	AX482567	Sequence
39	916	52.9	2075	6	AX565707	Sequence
40	916	52.9	2075	6	AX597107	Sequence
41	916	52.9	2075	6	AX701365	Sequence
42	916	52.9	2075	8	AF001900	Homo sapi
43	916	52.9	4469	6	CS025753	Sequence
44	916	52.9	4469	6	AX236302	Sequence
45	916	52.9	4469	6	AX578081	Sequence

ALIGNMENTS

RESULT 1	BC050435	1852 bp	mRNA	linear	PRI 18-JUL-2005
LOCUS	BC050435				
DEFINITION	Homo sapiens secreted frizzled-related protein 5, mRNA (CDNA clone MG5.54179 IMAGE:6189478), complete cds.				
ACCESSION	BC050435				
VERSION	BC050435.1	GI:29791957			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,K.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stachenko,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uedlin,T.B., Toshitsuki,S., Carinci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richard,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huliyil,S., Villalon,D.K., Muzny,D.M., Sodergren,E.U., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,				
AUTHORS	1 (bases 1 to 1852)				

Db 276 GCGCTGACATGGGCGCGCGCGCTGCGAGAGTACGACTACTATGCTGGCAGGCCGAG 335
Qy 41 ProleuH1eG1A1yArSerTySerLySProProG1nCySleuAaP1leProA1aAaPleu 60
Db 336 CCGCTGCACGGCGGCTCTTACTCCAAAGCCGCGCAGTGGCTTGAATCCCTGGCGACCTG 395
Qy 61 ProleuCyH1eThVa1G1yTyLyBaRMeTaRLeuProAaP1leuG1uH1eG1u 80
Db 396 CCGCTGCGACACGCTGGGCTTCAAGCCGATCCGCTGCCCAACCTGCTGGAGCAGAG 455
Qy 81 SerLeuA1aG1uValLySvG1nG1nA1aSerSerTyRLeuProleuAaP1leAaRyCyS 100
Db 456 AGCTTGCGCGAGTGAAGCAGCAGCGAGAGAGCTGGCTGCCCTGGCCAGAGCCCTGC 515
Qy 101 H1eSerAaP1ThR1nVa1PheLeuCySserLeuPheA1aProVa1CySleuAaP1aPPro 120
Db 516 CACTGGATACGAGAGTCTTCTGCTGCTGCTTTGGCGCGCTGCTGCTGCTGCTGCTGCTG 575
Qy 121 H1eTyRProCyAaRSerLeuCySvG1uA1aVa1aRyA1aG1yCySvA1aPProleuMetG1u 140
Db 576 ATCTACCCGCTGCGCTGCTGCTGCGAGCGCGCTGCGCGCGCTGCGCGCTGCTGCTGAG 635
Qy 141 A1aTyRg1yPheProTTPProG1uMeTLeuH1eCySvH1eSvPheProleuAaP1aAaP 160
Db 636 GCTTACGCTTCCCTGCGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695
Qy 161 LeuCySv1aA1aVa1G1nPhG1yH1eSvProA1aThR1aPProVa1ThRyS1e 180
Db 696 CTCTGCATCGCGCTGCGAGTTCGGGCACTGCGCGCGCGCTGCGCGCTGCGCGCTGCGAG 755
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Db 876 ATTGAGGCCCAAGAAAAGAAAGAGCTGCTCAAGCCGCGCGCTGAGAGCGCAAGCAGC 935
Qy 241 LySvA1aG1uValLySvH1eSvMeTlySvAaP1yA1aG1yCySvProCySvProG1nLeuAaP1Ser 260
Db 936 AAGCGGCTGCTGCTGCACTGAAGAAATGGCGCGCGCTGCGCTGCGCGCGCTGCGAGCAGC 995
Qy 261 LeuA1aG1ySerPheLeuValMeTg1yA1aRySvValAaP1yG1nLeuLeuMeTg1a 280
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Qy 281 ValTyRg1yThR1aP1ySvLySvAaP1yG1uMeTlySvPheA1aValLySvPheMeTPheser 300
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Qy 301 TyRProCySvSerLeuTyRProPhePheTyRg1yA1aA1aG1uProH1e 317
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RESULT 4
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LOCUS AX597116 1984 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 77 from Patent WO02090992.
ACCESSION AX597116
VERSION AX597116.1 GI:28397671
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Andrews, P., Draper, J. and Walsh, J.
TITLE Screening method

JOURNAL Patent: WO 02090992-A 77 14-NOV-2002;
Axordia Limited (GB)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 1,726-141 Length: 1984
Score: 1730.00 Matches: 317
Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
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Qy 21 A1aLeuH1eThR1aA1aProA1aRySvG1uG1uTyR1aP1yTyRg1yThRg1nA1aG1u 40
Db 276 GCGCTGACATGGGCGCGCGCGCGCTGCGGAGCGCGCGCTGCGCTGCTGCGGCGAG 335
Qy 41 ProleuH1eG1A1yArSerTySerLySProProG1nCySleuAaP1leProA1aAaPleu 60
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Db 396 CCGCTGCGACACGCTGGGCTTCAAGCCGATCCGCTGCCCAACCTGCTGGAGCAGAG 455
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Db 456 AGCTTGCGCGAGTGAAGCAGCAGCGAGAGAGCTGGCTGCCCTGGCCAGAGCCCTGC 515
Qy 101 H1eSerAaP1ThR1nVa1PheLeuCySserLeuPheA1aProVa1CySleuAaP1aPPro 120
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Qy      301 TYrProCysSerLeuTYrTYrProPhePheTYrGlyAlaAlaGluProHis 317
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LOCUS      Sequence 38 from Patent WO03012082.
DEFINITION      AX701369
ACCESSION      AX701369
VERSION      AX701369.1 GI:29537018
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE
  1 Andrews, P., Walsh, J. and Gokhale, P.
  AUTHORS      Method for modulating stem cell differentiation using stem loop rna
  TITLE      Patent: WO 03012082-A 38 13-FEB-2003;
  JOURNAL      Axordia Limited (GB)
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Pred. No.:      1,72e-141      Length:      1984
Score:          1730.00      Matches:      317
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:            6      Gaps:      0

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Qy      41 ProLeuHisGlyArgSerTYrSerLysProProGlnCysLeuAspIleProAlaAspLeu 60
Db      336 CCGCTGCACGCGCGCTCTACTCCAGCCGCCGACAGCTTGACATCCCTGCCGACCTG 395
Qy      61 ProLeuCysHisThrValAlaGlyTYrLysArgMetArgLeuProLeuLeuGluHisGlu 80
Db      396 CCGCTGTGCACACGGGGGCTACCAAGCGCATCGGCTGCCCAACCTGTGGAGACAGAG 455
Qy      81 SerLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCys 100
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Qy      101 HisSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgPro 120
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Db      576 ATCTACCGCTGGCGCTGTGTGGAGCGGTGGCGCCGACGCTGGCGCGCTCATGGAG 635
Qy      141 AlaTYrGlyPheProTrpProGluMetLeuHisCysHisValPheProLeuAspAsnAsp 160

Db      636 GCTTACCGCTCCCTGCGCTGAGATGCTGCACCTCCACCAAGTTCCCTTGGACACAGAC 695
Qy      161 LeuCysIleAlaValGlnPheGlyHisIleuProAlaThrAlaProValThrIysIle 180
Db      696 CTCTGCATGCCCTGTGACATTCGGGACCTGCCCGCCACCGGCTCTCCATGACCAAGATC 755
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Db      1116 TACCCCTGCTCCCTCTACTACCTCTTCTTCTTCTACGGGGCGGACAGAGCCCCAC 1166

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AF017988      1984 bp      mRNA      linear      PRI 29-JUL-1999
LOCUS      Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA,
DEFINITION      complete cds.
ACCESSION      AF017988
VERSION      AF017988.1 GI:2415418
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE
  1 (bases 1 to 1984)
  AUTHORS      Melkonyan, H.S., Chang, W.C., Shapiro, D.P., Mahadevappa, M.,
  TITLE      Fitzpatrick, P.A., Kiefer, M.C., Tomei, L.D. and Umansky, S.R.
  JOURNAL      SARPs: a family of secreted apoptosis-related proteins
  PUBLISHED    Proc. Natl. Acad. Sci. U.S.A. 94 (25), 13636-13641 (1997)
  9391078
  2 (bases 1 to 1984)
  AUTHORS      Melkonyan, H., Prochazka, V. and Umansky, S.R.
  TITLE      Direct Substitution
  JOURNAL      Submitted (11-AUG-1997) LXR Biotechnology, Inc., 1401 Marina Way
  SOUTH, Richmond, CA 94804, USA
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 DEFINITION Sequence 6519 from Patent WO20068579.
 ACCESSION CQ720585
 VERSION CQ720585.1 GI:42281442
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 TITLE Kite, such as nucleic acid arrays, comprising a majority of
 humenexons or transcripts, for detecting expression and other uses
 thereof
 JOURNAL Patent: WO 02068579-A 6519 06-SEP-2002;
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Qy	301	TyPProCySerLeuTyTyTyProPhePheTyG1YalA1aG1uProH1s	317
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DEFINITION	Novel human gene analogous to secretory mouse protein sFRP-1.		
ACCESSION	E44023		
VERSION	E44023.1	GI:18625175	
KEYWORDS	JP 2000106889-A/1.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1280)		
AUTHORS	Fu, A. and Zu, Y.		
TITLE	Novel human gene analogous to secretory mouse protein sFRP-1		
JOURNAL	Patent: JP 2000106889-A 1 18-APR-2000; SMITHKLINE BEECHAM CORP		
COMMENT	OS Unidentified PN JP 2000106889-A/1 PD 18-APR-2000 PF 10-SEP-1999 JP 1999256823 PR 08-APR-1997 US 08/907808, 23-MAY-1997 US 60/047691 PI ADINGU FU YUN ZU PC C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395, PC A61K39/395, A61K45/00, PC A61K48/00, A61P3/04, A61P3/10, A61P9/00, A61P9/12, A61P13/12, PC C07K14/47, PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, PC C12O1/02, C12O1/68, PC G01N33/53, G01N33/531, G01N33/566, G01N33/577//C12P21/08, PC C12N15/00, A61K37/02, PC C12N5/00 CC Serendness: Single; CC Topology: Linear; FH key FT source FT Location/Qualifiers 1. 1280 /organism='Unidentified'. Location/Qualifiers 1. 1280 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"		
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[illegible]

Goodman, B., Ratner, A., Moody, S., Stetten, G., Campochiaro, P.A. and Zack, D.J.
Cloning and characterization of a secreted frizzled-related protein that is expressed by the retinal pigment epithelium
Hum. Mol. Genet. (1999) In press
2 (bases 1 to 1728)
Chang, J.T., Baum, N., Campochiaro, P.A. and Zack, D.J.
Direct Submission
Submitted (05-JAN-1999) Ophthalmology, JHMI, 809 Maumenee, 600 N. Wolfe St., Baltimore, MD 21287-9289, USA

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IAVQGHLPATAPVTKI CAOCSEMSHSDGMEOMCSDFVYKMIKEIKIENGRLK
IGAKKKLTKSGPLKRDTRILVYHMKNSACPCPOLDSLAGSLVNGRKVDGLLL
MAVIRWDXKNEMKFAVKFMFSYPCSLYIPFYGAAPRH"

ORIGIN

Alignment Scores:

Pred. No.: 4.37e-135 Length: 1728
Score: 1656.00 Matches: 305
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 8
Query Match: 95.7% Indels: 0
DB: 4 Gaps: 0

US-10-768-566-1 (1-317) x AF117757 (1-1728)

QY 5 ALaalaaglygylvalargthralaaleuialeuileuiglyalaaleuhsrtp 24
DB 41 GCGGCGCGCGGCGCGCGCGCGCGCGCTGCTGCTGCTGCGGCGCTGCAACGG 100
QY 25 AlaProlaAArgCyegluGluGlyTraspyrTYrGlyTTPGlnAlaGluProleuhsrly 44
DB 101 GCGCGCGCGCGCGCGGAGGAGTACACTACGCGCTGGCAGACGCGCGCTGACCGGG 160
QY 45 ArgSerTYrSerIyProProGlnCySleuAAspIleProAlaAspLeuProleuCyshs 64
DB 161 CGCTGCTACTCCAGACCGCCGCCAGTGCCTGCACTCCCGCGACCTGCGCTGCGCAC 220
QY 65 ThrValGlyTYrLyshArgWethArgleuProAenleuLeuGluhsrlyserleuAaglu 84
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QY 105 GlnValAlpHeuCySerSerIyheuAlaProValCySleuAAspIleProIleTyPProCyS 124
DB 341 CAGGCTCTCTGCTGCTGCTCTTCCGCCCGCTGCTGCTGCAACCGGCCACTACCTTGC 400
QY 125 ArgSerLeuCyegluAlaValArgAaglyCySalaProleuMetGlnAlaTyrglyPhe 144
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QY 165 GlnMetGluhsrIleSerAlaAspGlyLeuMetGluGlnMetCySerSerAspPheVal 204
DB 561 GAGATGGAGCAGAGCTGCGAGCTCACTGAGCAGAGATGTCTCCAGGACCTGCTGTC 640
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DB 701 AAAAGAGAGAGCTGCTCAAGTCCGCGCCCTGGAAGCGCAAGACACCAAGAGGCTCGTG 760
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QY 285 AspLyshLyshsnLyshGluMetLyshPheAlaValLyshPheMetPheSerTyPProCySer 304
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QY 305 LeuTYrTYrProPhePheTYrGlyAlaAlaGluProhs 317
DB 941 CTTACTACCCCTCTCTCTATGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979

RESULT 11
BC032921

LOCUS BC032921 1813 bp mRNA linear ROD 25-JUL-2005
DEFINITION Mus musculus secreted frizzled-related sequence protein 5, mRNA
(CDNA clone MGC:41101 IMAGE:1395864), complete cde.

ACCESSION BC032921
VERSION BC032921.1 GI:21411182

KEYWORDS MGC.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 1813)
Straube, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Ditschenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Cabavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Tomihata, S.,
Carinci, P., Prange, C., Raha, S.S., Loquelelano, N.A., Peters, G.J.,
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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Hellon, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalka, U., Smilins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Herrera, M.A.

CONSTRM

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PUBMED
12477932

REFERENCE
AUTHORS
CONSTRM
TITLE
NIH MGC Project
Direct Submission

Mangun,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhinney,S., McLeod,M., Mcneill,T., Meenen,E., Milosavljevic,A.,
Miwier,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
Morris,S., Mundasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
Newton,N., Nguyen,N., Norris,S., Nwaelelemeh,O., Okunnu,G.,
Olanupinsoo,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Polndexter,A.,
Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quroz,J., Rachlin,B.,
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
Reuter,M., Richards,S., Riggs,F., Rivers,C., Rockey,T., Rojas,A.,
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savary,G., Scherer,S.,
Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
Song,X.-Z., Sorelle,R., Soosa,J., Steimle,M., Strong,R., Sutton,A.,
Svatek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
Tingey,A., Trejos,Z., Uemami,K., Valas,R., Vera,V., Villaseana,D.,
Waldron,L., Walker,B., Wang,J., Wang,O., Wang,S., Warren,J.,
Warren,R., Wei,X., White,F., Williams,G., Wilson,R., Wleczka,R.,
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 210385)
Worley,K.C.

Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 210385)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 210385)
Worley,K.C.

Direct Submission
Submitted (30-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 30, 2003 this sequence version replaced gi:30580782.
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
it will be indicated in the annotation.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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62. .246
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complement(626. .760)
/rpt_family="B1F"
complement(2022. .2139)
/rpt_family="PB1D9"
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repeat_region 3769. .3857
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OY	202	-----	202
Dd	94550	CCACTAGCTTAAGSGCTCCGCGTCCCTAAGCAAAATNGATTCCTTCTGTACCATCTTTG	94491
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Dd	94490	CAAACCTTTCACACAGTGTGTCAAAATGCGCATTTAAGAAGATCAAGATAGCAATAAGGGAGCC	94430
OY	218	rGlYvSlEUilleglVAlAgInLyBLYbvylsvElumEuySPProGIYProlEuLYARGL	238
Dd	94430	GCAA GTT GAT T GG AG C CC CA A GA A GA A G A GC TG CT CA A G SC A GS GCC CCT TT AA AC CG CA	94370
OY	238	ySAAPTRILysrLeJueIVallEHniEmeCyBsAnGlylaGIcySProCYsPROGINL	258
Dd	94370	AGGACACCAAGAACACTGTTCTTGCACTGAAGAAGCGGGCACGCTCCCCCTGCCCACT	94310
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Dd	94310	TAGCAACACTGACAGGAGACTTCCTGTGATGGSCCGCAAAAGTGAAGGACAGCTGCTGC	94251
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Dd	94190	TGTTCTCTTACCCTGTCTCCCTCTACTACACCTTTTTTCATTGSGGCAGACTGAACCCAC	94132
RESULT 14			
LOCUS	AC119236/c	163348 bp	DNA linear ROD 01-OCT-2003
DEFINITION	Mus musculus chromosome 19, clone RP24-213B12, complete sequence.		
ACCESSION	AC119236		
VERSION	AC119236.8	GI:33285101	
KEYWORDS	HMG.		
SOURCE ORGANISM	Mus musculus (house mouse)		
REFERENCE AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleia; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 163348) Bliren,B., Nusbbaum,C. and Lander,E. Mus musculus chromosome 19, clone RP24-213B12 unpublished 2 (bases 1 to 163348) Bliren,B., Linton,L., Nusbbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barua,N., Bastien,V., Bloom,T., Boguslavsky,I., Bookhalter,B., Brown,A., Camarota,J., Campotiano,A., Chang,D., Chkatzo,B., Chopel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A., Cooke,P., Dekrelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goylete,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K., Lamazares,F., Landers,T., Lehoczky,J., Levine,R., Liacouge,K., Lamazares,F., Landers,T., Lehoczký,J., Levine,R., Liacouge,K., Lamazares,F., Maclean,C., MacDonald,P., Major,J., Margulis,N., Matthews,C., McCarthy,M., Mcwan,P., McKernan,K., Meldrim,J.Y., Meneus,L., Milhov,T., Mlenka,V., Murphy,T., Naylor,U., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,W., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnapack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stanjanovic,N., Strauss,N., Subramanian,A., Talamaas,J., Testley,S., Theodore,J., Tophan,K., Travers,M., Travis,N., Triffillo,U., Vassilev,H.,		

TITLE	Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.
JOURNAL	Direct Submission
REFERENCE	Submitted (325-APP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	3 (bases 1 to 163348)
Birren, B., Nusbaum, C., Lander, E., Abouelellail, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, Y., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erikson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, U., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Rachukpa, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilleev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.	
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	4 (bases 1 to 163348)
Birren, B., Nusbaum, C., Lander, E., Abouelellail, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, Y., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erikson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, U., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Rachukpa, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilleev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.	
TITLE	Direct Submission
JOURNAL	Submitted (26-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	5 (bases 1 to 163348)
Birren, B., Nusbaum, C., Lander, E., Abouelellail, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, Y., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erikson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, U., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, X., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Rachukpa, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilleev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.	
TITLE	Direct Submission
JOURNAL	Submitted (26-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	5 (bases 1 to 163348)
Birren, B., Nusbaum, C., Lander, E., Abouelellail, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, Y., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erikson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, U., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, X., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Rachukpa, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilleev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zempek, L., Zimmer, A. and Zody, M.	

TITLE	Wyman,D., Young,G., Zaitoun,J., Zenbek,L., Zimmer,A. and Zody,M.
JOURNAL	Direct Submission Submitted (01-OCT-2003) Whitehead Institute/MIT Center for Genom Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 26, 2003 this sequence version replaced gi:32401630. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
COMMENT	-- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information ----- Center project name: L25239 Center clone name: 213_B_12 -----
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 LOCUS AL603804
 DEFINITION Mouse DNA sequence from clone RP23-470C16 on chromosome 11,
 complete sequence.
 ACCESSION AL603804.18 GI:21998175
 VERSION AL603804
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 189196)
 AUTHORS Harrison, E.
 TITLE Direct Submision
 JOURNAL Submitted (07-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Jul 26, 2002 this sequence version replaced gi:21955486.
 COMMENT
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones.
 where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submision
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., paired quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 06:51:33 ; Search time 682 Seconds
(without alignments)
3097.812 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAAGCVRTAATALLG.....MFSYPCSLTYPPFYGAEPH 317

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 segs, 333346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1730	100.0	954	9	ADA38290 Human sec
2	1730	100.0	1905	9	ADA38288 Human sec
3	1730	100.0	1905	12	ADM66969 Human hom
4	1730	100.0	1905	13	ADP56061 Human PRO

SUMMARIES

5	1730	100.0	1984	2	AAV19114	AAV19114 Human sec
6	1730	100.0	1984	8	ABX75334	ABX75334 Human CDN
7	1730	100.0	1984	8	AAD52563	AAD52563 SARP 3 DN
8	1730	100.0	1984	8	ABZ81835	ABZ81835 FRPHE nuc
9	1692	97.8	1280	2	AAV08946	AAV08946 Human ARG
10	1613	93.2	945	8	ADA38293	ADA38293 Mouse sec
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45	1613	93.2	1186	9	ADA38291	ADA38291 Mouse sec

ALIGNMENTS

RESULT 1	ADA38290	ADA38290 strand; cDNA; 954 BP.
ID	ADA38290	ADA38290 strand; cDNA; 954 BP.
XX	ADA38290	ADA38290 strand; cDNA; 954 BP.
AC	ADA38290	ADA38290 strand; cDNA; 954 BP.
XX	ADA38290	ADA38290 strand; cDNA; 954 BP.
DT	20-NOV-2003	(first entry)
XX	20-NOV-2003	(first entry)
DE	Human secreted apoptosis related protein (SARP) 3 cDNA coding region.	
XX	Human secreted apoptosis related protein (SARP) 3 cDNA coding region.	
KW	Human; ss; gene; metabolic disorder;	
KW	Secreted Apoptosis-Related Proteins 3; SARP3; obesity; overweight;	
KW	diabetes; insulin resistance; cachexia; anorexia; beta-catenin; leptin;	
KW	insulin sensitivity; food intake; body weight change; glucose tolerance;	
KW	hyperplastic growth; cell differentiation; programmed cell death;	
KW	apoptosis; hypertrophic growth; modulator; agonist; antagonist;	
KW	antitense; ribozyme; lipid; glucose; insulin; adipocyte; differentiation;	
KW	adipose cell; adipocyte; anorectic; antidiabetic; immunomodulator.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	1..954
FT	FT	/*tag= a
XX	FT	/product= "SARP3"
XX	US2003143610-A1.	

PD 31-JUL-2003.
XX 08-JAN-2003; 2003US-00338604.
PF 08-JAN-2002; 2002US-0346523P.
PR (MILL-) MILLENNIUM PHARM INC.
XX
PA Xu H;
PI WPI: 2003-635956/60.
DR P-PSDB; ADA38289.
XX
PT Identifying a compound for treating a metabolic disorder, e.g., diabetes
PT by assaying the ability of the compound to modulate a secreted Apoptosis-
PT Related Proteins 3 (SARF3) nucleic acid expression or polypeptide
PT activity.
XX
XX Disclosure; SEQ ID NO 3; 35PP; English.
XX
XX The invention discloses a method for identifying a compound for treating
CC a metabolic disorder which comprises assaying the ability of the compound
CC to modulate secreted Apoptosis-Related Proteins 3 (SARF3) nucleic acid
CC expression or polypeptide activity. Also claimed are methods for
CC modulating SARF3 mediated metabolic activity, treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity and a pharmaceutical formulation for
CC treating metabolic disorders. The metabolic disorders comprise obesity,
CC overweight, diabetes, insulin resistance, cachexia or anorexia. The
CC ability of the compound to modulate SARF3 nucleic acid expression or
CC polypeptide activity is determined by detecting a SARF3 activity of a
CC cell, or by detecting modulation of the level of beta-catenin, leptin or
CC insulin sensitivity, food intake, body weight change, glucose tolerance,
CC hyperplastic growth, cell differentiation, programmed cell death or
CC hypertrophic growth. Modulating SARF3 mediated metabolic activity
CC comprises contacting a cell or tissue expressing the SARF3 with a SARF3
CC modulator. The compound or modulator comprises a small molecule SARF3
CC agonist or antagonist or inverse agonist, anti-SARF3 antibody, antisense
CC SARF3 molecule or ribozyme. The SARF3 mediated metabolic activity
CC comprises the ability to modulate lipid, glucose or insulin metabolism,
CC adipocyte growth, the differentiation of adipose cell progenitors into
CC adipocytes or programmed cell death. Treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity comprises administering a SARF3
CC modulator. The compound is an oligonucleotide encoding an antisense or
CC ribozyme molecule that targets SARF3 transcripts and inhibits translation
CC or an oligonucleotide that forms a triple helix with the promoter of the
CC SARF3 gene and inhibits transcription. The sequence presented is the
CC human SARF3 cDNA coding region.
XX
SQ Sequence 954 BP; 171 A; 313 C; 308 G; 162 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,41e-163 Length: 954
Score: 1730.00 Matches: 317
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0
US-10-768-566-1 (1-317) x ADA38290 (1-954)
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DB 1 ATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
QY 21 AlaLeuHisTTrAlaProAlaArgCysGluGluTyrThrTyrTyrGlyTyrGlnAlaGlu 40
DB 61 GGGCTGCACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 41 ProLeuHisGlyArgSerTyrSerTyrProProGlnCysLeuAspTrpAlaAspLeu 60
DB 121 CGGTCGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180

QY 61 ProLeuCyHisThrValGlyTyrIlyArgMetArgLeuProAsnLeuLeuGluHisGlu 80
DB 181 CGGCTCTCCACACCGGTGGGCTTACAGCGCATGCGGCTGCCAACCTCTGGAGACGAG 240
QY 81 SerLeuAlaGluValIlyGlnGlnAlaSerSerTProLeuLeuAlaIlyArgCys 100
DB 241 AGCCTGGCGGAGTAAACAGACAGGCGAGCTGGCGCTGGCGCTGGCCAAAGGCTGC 300
QY 101 HisSerAspThrGlnValPheLeuCySerSerLeuPheAlaProValCysLeuAspArgPro 120
DB 301 CACTCGGATACGACAGTCTTCTGTGCTCGCTCTTGGGCGGCTGTGTCTGACCGGCC 360
QY 121 IlyTyrProCyArgSerSerLeuCyGlnAlaValAlaArgAlaGlyCysAlaProLeuMetGlu 140
DB 361 ATCTACCGGTGGCGGCTCGCTGGCGAGGCGGCGGCGGCGGCTGGCGGCTGAG 420
QY 141 AlaTyrGlyPheProTyrProGluMetLeuHisCyHisIlyPhePheProLeuAspAsnAsp 160
DB 421 GCTTACGGGCTTCCCTGGCGCTGAGATGCTGCACGACAAAGTTCCCTGGACAAAGAC 480
QY 161 LeuCyHisAlaValAlaGlnPheGlyHisIlyAspProAlaThrAlaProProValThrIlyIle 180
DB 481 CTCTGCACTCGGCTGCACTTGGGCGACCTGGCGGCGGCGGCTTCCAGTACCAAGATC 540
QY 181 CysAlaGlnCyGluMetGluHisSerAlaAspGlyLeuMetGluGluMetCysSerSer 200
DB 541 TCGGCCAGGTGATGATGAGACACAGTGTGCTGATGACAGACATGTGCTCCAGT 600
QY 201 AspPheValValIlyMetMetArgIlyIlyGluIlyIlyIlyGlnAlaGlnAlaAspArgIlySer 220
DB 601 GACTTGTGGTCAAAATCGCATCAAGAGATCAAGATGAGATGGGAGACCGGAAAGCTG 660
QY 221 IlegIyAlaGlnIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 240
DB 661 ATTGAAGCCCAAAAGAAAGAAAGTGTCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 241 IlyArgLeuValIlyHisMetIlyAsnGlyAlaGlyCysProCyArgProGlnLeuAspSer 260
DB 721 AGCGGCTGGTGTCTGCATGAAAGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 261 LeuAlaGlySerPheLeuValMetGlyIlyArgValAlaArgIlyGlnLeuLeuMetAla 280
DB 781 CTGGGGGCGACGTTCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 281 ValTyrArgTyrAspIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 300
DB 841 GTCTACCGCTGGGACAAAGAAATTAAGAGATGAAGTTTGCAGTCAATTCATGTCTTCC 900
QY 301 TyrProCySerSerLeuTyrTyrProPhePheTyrGlyAlaAlaGluProHis 317
DB 901 TACCCCTGCTCCTCTACTACCTTTCTTTTACGCGGCGGCGGAGAGACCCAC 951
RESULT 2
ADA38288
ID ADA38288 standard; cDNA, 1905 BP.
AC
XX
AC ADA38288;
XX
DT 20-NOV-2003 (first entry)
XX
XX Human secreted apoptosis related protein (SARF) 3 cDNA.
DE
XX Human; ss; gene; metabolic disorder;
XX Secreted Apoptosis-Related Proteins 3; SARF3; obesity; overweight;
XX diabetes; insulin resistance; cachexia; anorexia; beta-catenin; leptin;
XX insulin sensitivity; food intake; body weight change; glucose tolerance;
XX hyperplastic growth; cell differentiation; programmed cell death;
XX apoptosis; hypertrophic growth; modulator; agonist; antagonistic;
XX antisense; ribozyme; lipid; glucose; insulin; adipocyte; differentiation;
XX adipose cell; adipocyte; anorectic; antidiabetic; immunomodulator.
XX
OS Homo sapiens.

KW		adipogenesis; hypertension; cardiovascular disease; anorectic;
KX		antidiabetic; hypotensive; sFRP-5; gene.
XX		
OS	Homo sapiens.	
PV	MO200401618-A2.	
PN		
XX		
PD	05-FEB-2004.	
PF	29-JUL-2003; 2003WO-US023684.	
PR	29-JUL-2002; 2002US-0398785P-	
PR	12-JUN-2003; 2003US-0478206P.	
PA	(HMGE-) HMGENE INC.	
PI	Chada K, Chouinard R, Ashar H, Sayed AMD;	
DR	MP1: 2004-143846/14. P-PDB: ADM67242.	
PT	Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue of mice of different genotypes.	
PS	Claim 11; SEQ ID NO 104; 91pp; English.	
XX		
CC	This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anti- obesity pharmaceutical compositions. Specifically, it refers to a high mobility group I-C protein (HMG-I-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMG-I-C -/-, Ob/Ob, or HMG-I-C +/- Ob/Ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and hypertensive activities. This polynucleotide sequence is a human homologue of a murine adipocyte specific DNA sequence of the invention.	
CC		
CC		
CQ	Sequence 1905 BP; 338 A; 610 C; 602 G; 355 T; 0 U; 0 Other;	
	Alignment Scores:	
	Pred. No.: 1.17e-162 Length: 1905	
	Percent Similarity: 1730.00 Matches: 317	
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	DB: Gaps: Indels: 0	
	US-10-768-566-1 (1-317) X ADM6969 (1-1905)	
OY	MetAAGAAAlAAAlAAAlAgIyGVAlAYGTThRAIAleuAlaleuleuEngly 20	
Dd	182 ATGGCGGCCGCAGCAGCGCGCGCGCGCGCTGCGACCGCGCGCTGCGCGCGG 241	
OY	AtAleuNHtAPrAlaPrAlaAAGCyAGUGLnTTyrAspRfTyTGITTPGlAnaIgLu 40	
Dd	242 GGcGTCACTTAGGGCGCGGGCGcCTCGAGAAGATAACAATTACTTAAGCTGGCKAGGCGAG 301	
OY	ProLeuNHlAgIYAgsERYTsETLYRPrcPGlnCYseuArPlleProAlaAprLeu 60	
Dd	302 CGGCTGCACAGCGCGCTCTACTCAAAGCCGCCAATGCTTCACATCCCTGCGAACSTG 361	
OY	ProLeuCVnhtHTThVAIGLyTYTLvARMeATgLeuPRAoleuAuLeuGIunhNglu 80	

Db	362	CCGCTCTGCGACACACG	TGGCGCTTACAAAGG	GCATGGGCGTGGCCAACTGCTGGAGCACAG	421
OY	81	SeTLeuAlAGlUaAllyAGlInGlnAlaSeSeT	TrPLeuProLeuLeuAlAlYbAlGyS	100	
Db	422	AGCTTGCGCGAAGTGAACAGCAGCGCAGCAG	CTGCTGCTGCGCTGCGCTGCGCGCAAGCGCTGC	481	
OY	101	HisSeTAspThGlnValPheLeuGySeSeT	PheAlaProValGySeLeuAspArgPro	120	
Db	482	CACTCGGATACGCAAGGCTCTTCCTGCTGCTGCT	CTTTGGCCGCGTGTGCTTGACCCGACC	541	
OY	121	IlLeTyrProGyAsArgSeTLeuCySeGlnAlaValAl	ArgAlaGyCybAlaProLeuMetGln	140	
Db	542	ATCTACCCGTCGCGCTCGCTGTGCGAAGCGCGG	CGCGCTGCGCGCGCTCATGTAG	601	
OY	141	AlaTyrGlyPheProTTPProGlnUeLeuHi	AcYbHiAlYbPheProLeuAspAsnAsp	160	
Db	602	GCCTAAGCGCTTCCCTGCGCTGAGATGCTGCA	CTGCCCAAGTTCCCTTGGAACAAGAC	661	
OY	161	LeuCyAlIeAlaValAlGlnPheGlyHisLeuProAl	aPTrAlaProProValThTyrIle	180	
Db	662	CTGTGATGCGCGGTGAGTTCGGAGACCTGCGC	CGCGACCGGCTGCCAGTGAACAATC	721	
OY	181	CyAlAGlCySeGlnUeGlnHiSeSeT	AlaAspGlyLeuMetGlnImeCySeSeT	200	
Db	722	TGGCGCCAGTGTGATGATGAGACACAGTCTCA	CGGCTCTCATGAGACAGATGTCTCCAGT	781	
OY	201	AspPheValIaValIyMetArgIleIyAGlnIle	IySAlIeGlnaAngIyaAspArgIyLeu	220	
Db	782	GACTTGTGTGGTCAAAATGTGGCATCAAGAGAT	CAAGATAGAGATGGGAGACCGGAAGCTG	841	
OY	221	IlAGlYAlAGlnIyAlYbIyAlYbLeuLeuIyS	ProGlyProLeuIyAlYbIyAlYbPThr	240	
Db	842	ATTGGAGCCCAAGAAAAGAAAGCTGTCAAGC	CGGCGCCCCCTGAAGCCCAAGACAC	901	
OY	241	IySArgIyLeuValIeUhiIyMetIySbAngIyAla	GlyCySProCySProGlnIyLeuAspSer	260	
Db	902	AAAGCGCTGCTGTGACATGAAGAAATGGCCG	GGCTGCCCCCTCCACAGCTGACACG	961	
OY	261	LeuAlAGlYSeTSePheLeuValIeGlnIyArgIy	AlaIySAlIeGlnIyLeuLeuMetAla	280	
Db	962	CTGGCGGGGCGCTTCCCTGCTCATGGCGCGCA	AGTGAATGAGACGCTGCTCATGGCC	102	
OY	281	ValTyrArgITrAspIyAlYbAlYbIyAGlUeT	IySPhenAlaValIySPhenMetPheSer	300	
Db	1022	GCTTACCGCTGGGACAAAGAAATGAAGATGA	AGATTGACGATCAATTCATGTTCTCC	108	
OY	301	TyrProCySeSerIyUtyTyrProPhePheTyr	GlyAlaIaIaGlnProHiS	317	
Db	1082	TACCCCTGCTCCCTCTACTACCTCTTTCTTCT	TCAACGGGCGGCGAGACCCCCAC	1132	
RESULT 4					
ADP56061	ADP56061 standard; cDNA; 1905 BP.				
XX	AC	ADP56061;			
XX	DT	18-NOV-2004 (first entry)			
XX	DE	Human PRO cDNA sequence SEQ ID NO:2037.			
XX	KW	human; PRO; immune related disease; inflammatory immune response;			
KW	KW	immune response stimulator; antidiabetic; antianflammatory; antiarthritic;			
KW	KW	antidiabetic; antidiabetic; antianflammatory; antiporiatic;			
KW	KW	antipneumatic; antithyroid; CNS; dermatological; gastrointestinal;			
KW	KW	haemostatic; hepatocrotic; immunostimulant; immunosuppressant;			
KW	KW	neurotropic; neuroprotective; osteopathic; respiratory; vasotropic;			
XX	XX	virucide; gene therapy; gene; ss.			
OS	XX	Homo sapiens.			
FN	XX	WO2004039956-A2.			
PD	XX	13-MAY-2004			

XX 14-NOV-2002.
 PD 29-APR-2002; 2002WO-GB001946.
 XX 04-MAY-2001; 2001GB-00011004.
 XX (AXOR-) AXORDIA LTD.
 PA Andrews P, Draper J, Walsh J;
 PI WPI: 2003-120579/11.
 XX P-PSDB; AAE34065.
 DR
 PT Identifying biologically active agents comprises cloning transfected
 PT cells into a cell array, exposing the array to an agent to be tested, and
 PT detecting signals generated by a reporter molecule as a result of
 PT exposure to the agent.
 XX
 XX Claim 19, Fig 81, 90pp; English.

XX The present invention relates to a novel screening method which enables
 CC the identification of biologically active agents which mediate their
 CC effect through the activation of genes. The method involves providing a
 CC population of cells stably transfected with a nucleic acid encoding a
 CC reporter molecule, cloning the transfected cells into a cell array,
 CC exposing the array to at least one agent to be tested and detecting a
 CC signal generated by the reporter molecule as a result of exposure to the
 CC agent. The method is useful in identifying biologically active agents and
 CC the genes through which the agents act, in screening potential drugs for
 CC their ability to activate certain drug targets in a high-throughput
 CC assay, in identifying relationships between signalling pathways and
 CC specific signals that could be useful in eventually directing the
 CC differentiation of embryonic stem cells and in toxicology assays by
 CC testing for unwanted activation or inhibition of specific signalling
 CC pathways. The present sequence is SARP 3 DNA used to illustrate the
 CC method of the invention. Note: This sequence is said to encode the
 CC sequence shown in Figure 82, but this does not appear to be the case
 CC
 XX SQ Sequence 1984 BP; 353 A; 634 C; 627 G; 370 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,24e-162 Length: 1984
 Score: 1730.00 Matches: 317
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0
 US-10-768-566-1 (1-317) x AAD52563 (1-1984)

QY 1 MetATGAlaAlaAlaAlaAlaGlyValArgThrAlaAlaAlaLeuAlaLeuLeuGly 20
 DB 216 ATGCGGGCG 275
 QY 21 AlaLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 40
 DB 276 GCGCTGACACG 335
 QY 41 ProLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
 DB 336 CCGCTGCG 395
 QY 61 ProLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
 DB 396 CCGCTGCG 455
 QY 81 SerLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 100
 DB 456 AGCTGCG 515
 QY 101 HisSerArgThrGlnValPheLeuGlySerLeuPheAlaProValCylLeuAspArgPro 120

DB 516 CACTGGATACGACAGCTCTTCTGTGCTCTTGTGGCGCCGCTGTGTGACCGGCC 575
 QY 121 IleTyrProCysArgSerLeuGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 140
 DB 576 ATCTACCCGCTCGCTCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 635
 QY 141 AlaTyrGlyPheProTyrProGlyMetLeuAlaCysAlaGlyPheProLeuAspAsp 160
 DB 636 GCTTACGGCTTCCCTGCGCTGAGATGCTGACCTGCGCAAGTTCCCTGACCAAGCAG 695
 QY 161 LeuCysIleAlaValAlaGlnPheGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 180
 DB 696 CTCTGACCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 755
 QY 181 CysAlaGlnCysGlyMetGlnHisSerAlaAspGlyLeuMetGlnMetCysSerSer 200
 DB 756 TGCGCCGAGTGTGATGAGACACAGTGTGACGCGCGCTGATGAGACAGATGTGCTCCAGT 815
 QY 201 AspPheValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 220
 DB 816 GACTTGTGTCAAAATGCGCATCAAGAGATCAAGATGAGATGAGATGAGATGAGATGAG 875
 QY 221 IleGlyAlaGlnCysGlyLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 240
 DB 876 ATTGAGCG 935
 QY 241 LysArgLeuValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 260
 DB 936 AAGCGCGTGTGCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 995
 QY 261 LeuAlaGlySerPheLeuValMetGlyValGlyValAlaAlaAlaAlaAlaAlaAlaAla 280
 DB 996 CTGGCG 1055
 QY 281 ValTyrArgTyrPheAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 300
 DB 1056 GTCTACCGCTGAGACAGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1115
 QY 301 TyrProCysSerLeuTyrTyrProPhePheTyrGlyAlaAlaAlaAlaAlaAlaAlaAla 317
 DB 1116 TACCGCTGCTCTCTACTACCTTTCTTCTACCGCGCGCGCGCGCGCGCGCGCGCG 1166

RESULT 8
 AB281835
 ID AB281835 standard; DNA; 1984 BP.
 XX
 AC AB281835;
 XX
 DT 11-JUN-2003 (first entry)
 XX
 DE FRPHE nucleic acid sequence.
 XX
 KW FRPHE; stem cell; stem-loop RNA; antianemic; cerebroprotective;
 KW neuroprotective; nootropic; antiparkinsonian; caritant; hepatotropic;
 KW antididetic; vulnerary; gene therapy; gene; ds.
 OS unidentified.
 XX
 PN MO2003012082-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 25-JUL-2002; 2002WO-GB003409.
 XX
 PR 26-JUL-2001; 2001GB-00018223.
 XX
 PA (AXOR-) AXORDIA LTD.
 XX
 PI Andrews P, Walsh J, Gokhale P;
 XX
 DR WPI: 2003-278398/27.
 XX
 PT Modulating the differentiation state of a stem cell, useful for treating

imbalance by determining ATG-1709 polypeptide expression levels. ATG-1709 polypeptides can be used to screen for agonists and antagonists which bind the ATG-1709 polypeptide. These can be used in treatment to activate or inhibit ATG-1709 activity, in addition to direct administration of antisense sequences to prevent expression, or ATG-1709 polypeptides to treat conditions associated with a lack of ATG-1709. Gene therapy may also be used to affect endogenous ATG-1709 expression. ATG-1709 antibodies are useful for inducing an immune response to immunise and prevent disease, and for isolating ATG-1709 clones or purifying the polypeptides by affinity chromatography. ATG-1709 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented or treated include: heart disease; hypertension; cardiovascular diseases; kidney disease; obesity; insulin resistance, diabetes and Central Nervous System (CNS) diseases. The ATG-1709 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.

SQ Sequence 1280 BP; 223 A; 417 C; 410 G; 230 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,236-159	Length:	12800
Score:	1692.00	Matches:	315
Percent Similarity:	99.4%	Conservative:	0
Best Local Similarity:	99.4%	Mismatches:	2
Query Match:	97.8%	Indels:	1
DB:	2	Gaps:	0

US-10-768-566-1 (1-317) x AAV08946 (1-1280)

QY		M e r F x R A l a l a l a l a l a l a g i y V A L a g T P r I a a l a t u w a l a t u e u l e u G l y 20
D b	99	A t t e g g g c g g c g g c g g c g g g g g c g g c g g a c g g c g a c t g g c g c t g t g g g 158
QY	21	A l a l e u h i s t r p l a P r o l a l a r g C y s g i n g i u t y r A s p T y r T r p G l n a l a g l u 40
D b	159	G C C C T G A C T G G C G C G G C G C T G C G A G A G T A C A C T A C T A T G G T G S C A G C C G A G 218
QY	41	P r o l e u H i B g l y A r g S e r T y r S e r l y s P r o P o g i n C y l e u A s p I l e P r o l a A s p l e u 60
D b	219	C C C C T G C A C G G C G C C C T C A C T C C A A G C C G C G C A G T G C C T T G A C A T C C C G C G A C C T G 278
QY	61	P r o l e u C y s H i s t r t h a l a g l y T y r l y s A r g M e t A r g l e u P r o A n l e u l e u G l n H i a g l u 80
D b	279	C C C C T T G C C A C A C G G T G G G C T T A C A N G C C A T G C G C C C C A A C T G C T G A G A C A G A G 338
QY	81	S e r l e u a l a g l u v a l y s g i n g l n a l a s e r S e r t r l e u P r o l e u l e u a l y s A r g C y s 100
D b	339	A G C C T G C C G A A G T A G A A G A C A G C A G G G G A G C A C T G C G C C G C T G G C C A A C G C G T G C 398
QY	101	H i s s e r A s p T h r t g l n a l P h e l e u C y s S e r l e u P h e a l a P r o v a l C y l e u A s p A r g P r o 120
D b	399	C A C T C G G A A T A C G A G G T C T T C C T G G C T G C A C T T T T G G C C C G C T G C T G C A C C G G C C C 458
QY	121	I l e T y r P r o C y s A r g S e r l e u C y s g i n u l a V a l A r g l a g l y C y s A l a P r o l e u M e t G l u 140
D b	459	A T C T A C C C G T G C C G C T C G C T G T G C A G G C C G C G C C G C G C G C T G C G C G C C T A T G A G 518
QY	141	A l l e T y r G l y P h e P r o T r p P r o G l u M e t l e u H i s C y s H i a l y s P h e P r o l e u A s p A s n A s p 160
D b	519	G C C T A A G G G C T T C C C C T G C G C T G A G A T G C T G A C - T G C C A C A A G T T C C C C T G A C A A G A C 577
QY	161	L e u C y s I l e a l a V a l g i n P h e g l y H i s l e u P r o a l a T h r a l a P r o P r o v a l T h r l y s I l e 180
D b	578	C T T G C A T G C C G T G A G T T C G A G C A C C T G C C C G C C A C G G C C C A C A G T A C C A A G A T C 637
QY	181	C y s A l a g l n C y s g l u M e t G l u H i s s e r a l a A s p G l y l e u M e t G l u g i n M e t C y s S e r 200
D b	638	T G G C C C A A G T G A G A T G A G A C A G T G T A C G G C C T C A T G A G A C A G A T G C T C C A G T 697
QY	201	A s p P h e V a l a l y s M e t a r g l l e l y s G l u l l e l y s I l e g l u a n g l y A s p A r g l y l e u 220
D b	698	G A C T T T G T G T C A A A T G C G A T C A A G A G A T C A A G A T A T G G A A T G G G A C C G A A G C T G 757

QY	221	ILGLIYALAGLInylslylsylLeuLeuLysPProGILPProLeuLysAlaGlyAspThr	240
Db	758	ATTGGAGCCCAAGAAAAAGAAAGAGTGGCTCAAGCCGGGCCCCCTGAAGCCGAGAACACC	81.7
QY	241	LysArgLeuValLeuHisMetLysAsnGlyAlaGlyCysProCysProGlnLeuAspSer	260
Db	818	AAAGCGGTGGTGGTGCACATGAAGAAATGGCGGGGTGGCCCTGCCACAACTGGACAGC	87.7
QY	261	LeuAlaGlySerPheLeuValMetGlyArgIysValAspGlyGlnLeuLeuMetAla	280
Db	878	CTGGCGGGCAGCTTCTGGCTCAATGGCGCGCAAGGTGATGGACAGCTGGCTCATGGCC	93.7
QY	281	ValIysArgTyrAspLysLysAsnIysGlnMetLysPheAlaValLysPheMetPheSer	300
Db	938	GCTCAACGGCTGGGACAGAAAGAAATAGAAGATGAAGATTGGACATCAATTCAATCTTCC	99.7
QY	301	TyrProCysSerLeuTyrTyrProPhePheTyrGlyAlaAlaGluProHis	317
Db	998	TACCCCTGCTCCCTCACTACCTCTTCTTCAACGGGGGGGAGAACCCCAAC	104.8

RESULT 10

ADA38293
ID ADA38293 standard; cDNA; 945 BP

AC ADA38293;

DT 20-NOV-2003 (first entry)

DE Mouse secreted apoptosis related protein (SARP) 3 cDNA coding region.

KM Mouse; ss; gene; metabolic disorder;
KM Secreted Apoptosis-Related protein 3; SARP; obesity; overweight;
KM diabetes; insulin resistance; cachexia; anorexia; beta-catenin; leptin;
KM insulin sensitivity; food intake; body weight change; glucose tolerance;
KM hyperplastic growth; cell differentiation; programmed cell death;
KM apoptosis; hypertrophic growth; mediator; agonist; antagonist;
KM anisense; ribozyme; lipid; glucose; insulin; adipocyte; differentiation;
KM adipose cell; adipocyte; anorectic; antidiabetic; immunomodulator.

Musculus

Key	Location/Qualifiers
CDS	1..945
FT	/*tag= a
FT	/product= "SARP3"
FT	

PN US2003143610-A1

31-JUL-2003

PF 08-JAN-2003; 2003US-00338604.

PR 08-JAN-2002; 2002US-0346523P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Xu H.

DR WPI; 2003-635956/60

XX
XX

XXXXX, XXXXX - 7
XXXXX, XXXXX - 7

PT Identifying a compound for treating a metabolic disorder, e.g., diabetes
PT by assaying the ability of the compound to modulate a Secreted Apoptosis-
PT Related Proteins 3 (SARF3) nucleic acid expression or polypeptide
PT activity.

PS Disclosure; SEQ ID NO 6; 35pp; English.

CC The invention discloses a method for identifying a compound for treating
CC a metabolic disorder which comprises assaying the ability of the compound
CC to modulate Secreted Apoptosis-Related Proteins 3 (SARPs) nucleic acid
CC expression or polypeptide activity. Also claimed are methods for
CC modulating SARPs mediated metabolic activity, treating a subject having a

CC metabolic disorder characterised by aberrant SARP3 nucleic acid
 CC expression or polypeptide activity and a pharmaceutical formulation for
 CC treating metabolic disorders. The metabolic disorders comprise obesity,
 CC overweight, diabetes, insulin resistance, cachexia or anorexia. The
 CC ability of the compound to modulate SARP3 nucleic acid expression or
 CC polypeptide activity is determined by detecting a SARP3 activity of a
 CC cell, or by detecting modulation of the level of beta-catenin, leptin or
 CC insulin sensitivity, food intake, body weight change, glucose tolerance,
 CC hyperplastic growth, cell differentiation, programmed cell death or
 CC hypertrophic growth. Modulating SARP3 mediated metabolic activity
 CC comprises contacting a cell or tissue expressing the SARP3 with a SARP3
 CC modulator. The compound or modulator comprises a small molecule SARP3
 CC agonist or antagonist or inverse agonist, anti-SARP3 antibody, antisense
 CC SARP3 molecule or ribozyme. The SARP3 mediated metabolic activity
 CC comprises the ability to modulate lipid, glucose or insulin metabolism,
 CC adipocyte growth, the differentiation of adipose cell progenitors into
 CC adipocytes or programmed cell death. Treating a subject having a
 CC metabolic disorder characterised by aberrant SARP3 nucleic acid
 CC expression or polypeptide activity comprises administering a SARP3
 CC modulator. The compound is an oligonucleotide encoding an antisense or
 CC ribozyme molecule that targets SARP3 transcripts and inhibits translation
 CC or an oligonucleotide that forms a triple helix with the promoter of the
 CC SARP3 gene and inhibits transcription. The sequence presented is the
 CC mouse SARP3 cDNA coding region.

XX SQ Sequence 945 BP; 193 A; 304 C; 276 G; 172 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,2e-151 Length: 945
 Score: 1613.00 Matches: 295
 Percent Similarity: 96.5% Conservative: 5
 Best Local Similarity: 94.9% Mismatches: 11
 Query Match: 93.2% Indels: 0
 DB: 9 Gaps: 0

US-10-768-566-1 (1-317) x ADA38293 (1-945)

QY 7 AAGAGTGYVAlArGTThrAlaAlaLeuAlaLeuLeuGAlaAlaLeuHisThrAlaPro 26
 DB 10 GCGTGAAGGACGACGACGCGCGCTGCTGCTGCGGGCGCTGATGGGCGCA 69
 QY 27 AAtargCySgluGluTyrAspTyrTyrGlyTyrGlnAlaGluProLeuHisGlyArgSer 46
 DB 70 ACACGGCGGACAGAGTACGACTACTACGCTTGCGAGCGGACCGCTGACGGCGCTCC 129
 QY 47 TyrSerLysProProGlnCysLeuAspLysProAlaAspLeuProLeuCysHisThrVal 66
 DB 130 TACTCCAGGCCACCGCAGTGCCTCGACATCCCGCGCATCTGCGCTGTCAACAGGTG 189
 QY 67 GATYTYLVAATGMeTArGleuProAsnLeuLeuGluHisGluSerLeuAlaGluValLys 86
 DB 190 GCGTACAAAGCGATGGCTGCGCAACCTGCTGAGACAGAAAGCCTGGCCGAGGTGAAG 249
 QY 87 GlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCysHisSerAspThrGlnVal 106
 DB 250 CAGCAGGACAGAGCGTGGCTGCACCTGCGGCAAGCGCTGCACCTGACACCCAGGTG 309
 QY 107 PheLeuCySerLeuPheAlaProValCysLeuAspArgProIleTyrProCysArgSer 126
 DB 310 TTCCTCTGCTCGCTCTTCGCTCCGCTGCTGCGACCGACCATCTACCCCGCGCTCG 369
 QY 127 LeuCySgluAlaValArGAlaGlyCysAlaProLeuMeGluAlaTyrGlyPheProTyr 146
 DB 370 CTGTGCGAAGCTCGCGCGCGCGCTGCGCTGCATATGAGAGCTTACCGGTTCCCTTGG 429
 QY 147 ProGluMeLeuHisCysHisLysPheProLeuAspAsnAspLeuCysIleAlaValGln 166
 DB 430 CCCGAGATCTGCTGACCTGCAACAAGTTCCCGCTGACCAAGACTGTCGATCGCGGTGAG 489
 QY 167 PheGlyHisLeuProAlaThrAlaProProValThrLysIleCysAlaGlnCysGluLys 186
 DB 490 TTCGGGCACTGCTGCGCACCGCGCTCCAGTGACCAAGATCTGTGCTCCAGTGTGAGATG 549

QY 167 GlnHisSerAlaAspGlyLeuMeTGlGlnMeTysSerSerAspPheValValLysMet 206
 DB 550 GAGCACACGCGTGAACGCGCTCATGGACAGATGTCCTCAATGACTTTGTGTGTCAGATG 609
 QY 207 ArgIleLysGluIleLysIleGluAsnGlyAspArgLysLeuIleGlyAlaGlnLys 226
 DB 610 CGCATTAAGAGATCAAGATGACAAACGCGGACCGAAGTTGATTGGAGCCCAAGAGAG 669
 QY 227 LysLysLeuLeuLysProGlyProLeuLysArgLysAspThrLysArgLeuValLeuHis 246
 DB 670 AAGAACTGCTCCAAAGCGCGCGCTTAAAGCGCAAGACACCAAGAACTGTGCTGCAT 729
 QY 247 MetLysAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeu 266
 DB 730 ATGAAGAAACGGGGGACAGTGCCTTGCCCAATTAAGCAACTGACCGGACGAGCTTCCG 789
 QY 267 ValMetGlyArgLysValAspGlyGlnLeuLeuMeTAlaValTyrArgTrpAspLys 286
 DB 790 GTCAATGGCGCCCAAGTGAAGAGGACAGCTGCTGCACGGCGCTTACCGCTGGACAAAG 849
 QY 287 LysAsnLysGluMeLysPheAlaValLysPheMetPheSerTyrProCysSerLeuTyr 306
 DB 850 AAGAAATTAAGAGATGAAGTTGCGGTCAATTCATGTTCTCTATCCCTGTTCCCTTAC 909
 QY 307 TyrProPhePheTyrGlyAlaAlaGluProHis 317
 DB 910 TACCTTTTCTATAGGGGACGTGAACCCAC 942

RESULT 11

ADA38291
 ID ADA38291 standard; cDNA; 1186 BP.

XX ADA38291;

DT 20-NOV-2003 (first entry)

XX Mouse secreted apoptosis related protein (SARP) 3 cDNA.

XX Mouse; ss; gene; metabolic disorder;
 KW Secreted Apoptosis-related proteins 3; SARP3; obesity; overweight;
 KW diabetes; insulin resistance; cachexia; anorexia; beta-catenin; leptin;
 KW insulin sensitivity; food intake; body weight change; glucose tolerance;
 KW hyperplastic growth; cell differentiation; programmed cell death;
 KW apoptosis; hypertrophic growth; modulator; agonist; antagonist;
 KW antisense; ribozyme; lipid; glucose; insulin; adipocyte; differentiation;
 KW adipose cell; adipocyte; anorectic; antidiabetic; immunomodulator.

XX Mus musculus.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 242..1186

FT /*tag= a

FT /product= "SARP3"

PN US2003143610-A1.

XX 31-JUL-2003.

PD 08-JAN-2003; 2003US-00338604.

XX 08-JAN-2002; 2002US-0346523P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Xu H;

XX WPI; 2003-635956/60.

XX P-PSDB; ADA38292.

XX Identifying a compound for treating a metabolic disorder, e.g., diabetes

PT by assaying the ability of the compound to modulate a Secreted Apoptosis-

PT Related Proteins 3 (SARP3) nucleic acid expression or polypeptide

PT activity.

XX SQ Sequence 1755 BP, 245 A, 610 C, 585 G, 315 T, 0 U, 0 Other;
 Alignment Scores:
 Pred. No.: 2, 21e-87 Length: 1755
 Score: 977.00 Matches: 178
 Percent Similarity: 91.4% Conservative: 3
 Best Local Similarity: 89.9% Mismatches: 17
 Query Match: 56.5% Indels: 0
 DB: 14 Gaps: 0
 US-10-768-566-1 (1-317) x AEA18078 (1-1755)
 QY 1 MetATGAlaAlaAlaAlaAlaGlyValArgThrAlaAlaLeuAlaLeuLeuGly 20
 DB 1153 ATGCGGGCGGGCGGGCGGGGGGGCGTGCAGGACGGCGCTGGCGCTGGCGGG 1094
 QY 21 AlaLeuHisThrAlaProAlaArgCysGluGluTyrAspTyrTrpGlnAlaGlu 40
 DB 1093 GGGCTGCATGGCGCGCGCGCTGCAGAGAGTACAGTACTATGCTGGCAGCGCGAG 1034
 QY 41 ProLeuHisGlyArgSerTyrSerTyrProProGlnCysLeuAspIleProAlaAspLeu 60
 DB 1033 CGGCTGCAGCGCGCTGCCTTACTCAAGCGCGCACTGCTTACATCCCTGCCAGCTG 974
 QY 61 ProLeuCysHisThrValAlaGlyTyrTyrValArgMetArgLeuProAlaLeuGluHisGlu 80
 DB 973 CGGCTGCACACACGGTGGGCTACAGCCCATCGCGCTGCCAACCTGCTGGAGCAGAG 914
 QY 81 SerLeuAlaGluValArgGlnGlnAlaSerSerTrpLeuProLeuLeuAlaValArgCys 100
 DB 913 ACCCTGGCGGAAGTAAAGACAGCGAGCAGAGCTGCTGCTGGCCAAAGCCCTGC 854
 QY 101 HisSerAspThrGlnAlaPheLeuCysSerLeuPheAlaProValCysLeuAspArgPro 120
 DB 853 CACTCGGATCGCAGAGTCTTCTGCTGCTGCTTGGCCCGCTGCTGCTGCTGCTGCTGCTG 794
 QY 121 IleTyrProCysArgSerLeuCysGluAlaValArgAlaGlyCysAlaProLeuMetGlu 140
 DB 793 ACTACCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 734
 QY 141 AlaTyrGlyPheProTrpProGluMetLeuHisCysHisLeuPheProLeuAspArg 160
 DB 733 GCTTACGGCTTCCCTGGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 674
 QY 161 LeuCysAlaAlaValGlnPheGlyHisLeuProAlaThrAlaProProValThrIle 180
 DB 673 CTCTGATGCGCGCTGAGTTCGGGACCTGCCGCCACCGCGCTCAAGTAGCGCGCC 614
 QY 181 CysAlaGlnCysGluMetGluHisSerAlaAspGlyLeuMetGluGlnMetCys 198
 DB 613 GCGCGCGTCCCGCGCGCTCCAGCGCGCTGACAGTCCCTTACACAGCTCTGC 560
 RESULT 14
 AAV19115
 ID AAV19115 standard; DNA, 1308 BP.
 AC AAV19115;
 XX
 XX 28-ANG-1998 (first entry)
 DE Human secreted apoptosis-related protein hSARP2 DNA.
 KW Secreted apoptosis-related protein; SARP; hSARP2; human; prostate cancer;
 KW breast cancer; diagnosis; gene therapy; de.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 302..1246
 FT /*tag= a
 XX
 PN W09813493-A2.

XX 02-APR-1998.
 PD
 XX PF 24-SEP-1997; 97WO-US017154.
 XX PR 24-SEP-1996; 96US-0026603P.
 XX PR 11-OCT-1996; 96US-0028363P.
 XX PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 XX Umanaky S, Melkonyan H;
 XX WPI, 1998-230704/20.
 DR P-Psdb; AAW37817.
 PT New secreted apoptosis-related proteins - useful for modulating
 PT apoptosis, particularly for treatment of prostatic or breast cancer, also
 PT for diagnosis and monitoring of disease.
 PS Claim 2; Page 77-78; 101pp; English.
 XX
 CC This nucleic acid sequence encodes human secreted apoptosis-related
 CC protein hSARP2 (see AAW37817) that modulates apoptosis through cell-cell
 CC or cell-extracellular matrix signaling. hSARP2 cDNA was isolated from a
 CC human heart library, and hSARP1 (see AAV19113) and hSARP3 (see AAV19113)
 CC cDNAs were isolated from a human pancreatic library, using MSARP1 cDNA
 CC (see AAV19112) as probe. hSARP2 is expressed in most human tissues. It
 CC has pro-apoptotic activity. Once isolated, SARP nucleic acids can be
 CC expressed in usual vectors, either for use in gene therapy, or for
 CC recombinant SARP production. Antisense probes derived from SARP nucleic
 CC acids can be used in hybridisation tests for detecting levels of
 CC expression of SARP mRNA, particularly for diagnosis or monitoring of
 CC diseases associated with SARP expression. Specifically, they are used to
 CC detect cancer of the prostate or breast (by detecting hSARP1 or 2,
 CC respectively). SARP nucleic acids, polypeptides and antisense fragments
 CC can also be used to treat such cancers, or more generally apoptosis-
 CC related disease (e.g. infection with HIV or reperfusion injury), also
 CC (not claimed) to prevent apoptosis in cultured cells, to improve
 CC preservation of organs for transplantation, for in situ preservation for
 CC by-pass operations and to treat dermatological disorders
 XX
 SQ Sequence 1308 BP, 261 A, 416 C, 430 G, 201 T, 0 U, 0 Other;
 Alignment Scores:
 Pred. No.: 2, 61e-82 Length: 1308
 Score: 924.50 Matches: 179
 Percent Similarity: 72.8% Conservative: 51
 Best Local Similarity: 56.6% Mismatches: 77
 Query Match: 53.4% Indels: 9
 DB: 2 Gaps: 6
 US-10-768-566-1 (1-317) x AAV19115 (1-1308)
 QY 1 MetATGAlaAlaAlaAlaAlaGlyValArgThrAlaAlaLeuAlaLeu----- 18
 DB 302 ATGCGCATCGCGCGCGAGAGGGGGCGCGCGCGCGCGCGCGCTGGCGCTGGCGCG 361
 QY 19 LeuGlyAlaLeuHisThrAlaProAlaArgCysGluGluTyrAspTyrTrpGln 38
 DB 362 CTGGCGCGCGCGCTTGGCGCTGCGCGCTGCGCGCGAGTACAGTACTAGCTTCCAG 421
 QY 39 AlaGlu-----ProLeuHis---GlyArgSerTyrSerTyrProProGlnCysLeuAsp 55
 DB 422 TCGACATCGCGCGCTACAGAGCGGGCGCTTCAACCAAGCCACTCAGTGCCTGAGC 481
 QY 56 IleProAlaAspLeuProLeuCysHisThrValAlaGlyTyrValArgMetArgLeuProAsn 75
 DB 482 ATCCCCGGGAGCTTGGCTGGCCCAACGCTGCTACAGAAAGATGCTGCTGCCAAC 541
 QY 76 LeuLeuGluHisGluSerLeuAlaGluValArgGlnGlnAlaSerSerTrpLeuProLeu 95
 DB 542 CTGCTGGAGCAGAGACCATGGCGGAGGTAAAGCAGCAGCGCCAGCAGCTGGTGCCTTG 601

[illegible]

PA	(PROC) PROCTER & GAMBLE CO.
XX	Einstein R, White M, Bednarik D, Greene J, Doersen C;
PL	WPI; 2003-342664/32.
XX	P-PSDB; ABP72785.
DR	New isolated nucleic acid encoding a human secreted frizzled related
DR	protein, useful for preparing a composition for treating ischemic heart
XX	disease.
PT	disclosure; Page 47-49; 57pp; English.
PS	The present sequence is that of cDNA encoding human secreted frizzled
XX	related protein (sFRP). A variant sFRP cDNA (see AB262226) has been
CC	identified that is associated with ischemic heart disease. The variant
CC	sequence differs from the present sequence in having a C to G
CC	substitution altering the amino acid at position 174 of the encoding
CC	protein from Pro to Ala. The invention provides sFRP variant nucleic
CC	acid, vectors, host cells, and methods of producing the variant
CC	polypeptide. The variant sFRP nucleic acids and polypeptides can be used
CC	to identify agents which modulate the expression or activity of the
CC	polypeptide, to identify binding partners for the protein, to raise
CC	antibodies, and as diagnostic, prognostic and therapeutic agents for
CC	ischemic heart disease
SQ	Sequence 2094 BP; 484 A; 598 C; 631 G; 381 T; 0 U; 0 Other;
Alignment Scores:	
Pred. NO.:	5.07e-82 Length: 2094
Score:	924.50 Matches: 179
Percent Similarity:	72.8% Conservative: 51
Best Local Similarity:	56.6% Mismatches: 77
Query Match:	53.4% Indels: 9
DB:	8 Gaps: 6
US-10-768-566-1 (1-317) x AB262228 (1-2094)	
OY	1 MetcArgAlaAlaAlaAlaGlyGlyValArgThrAlaAlaLeuAlaLeu----- 18
Dd	303 ATGGGCATCGGGCGCAGCGAGGGGGGCCCGCGGGGACGCCCTCGGGCGTGTGGCG 352
OY	19 LeuGIvAlaLeuHieIrtPlAProAlaArgCysGluglutTyraapTYrTgLYtPrGln 38
Dd	363 CTGGGCGCGCGCTTCCTTGCGCGGTGGCTCGGCGCAAGTAGTACACTCGAGCTTCAG 422
OY	39 Alaglu-----Proleuhis---GLVtRgerTYseerLYsP-ProPGInCybleuAp 55
Dd	423 TCAGCATCGGCCCGCACAGACCGGGCGCTTTACACCAAGCACCCTCAGTGTGGAC 482
OY	56 IlAPoAlaAspLeuProleuCysHieThraAlGlyTYrLYsAtxMeLtaSgleuProAsn 75
Dd	483 ATCCCCGCGAACCTGGCGGTGTGCCACAACGTGGGCTACAAAGAAGATGTGCTGCCAAC 542
OY	76 LeuleuGluHieIslserleuAlaGluValLySGInGlnAlaserSerTPleuProleu 95
Dd	543 CTCCTGAGACACGAACCATGGCGAGGTGAAGACAGCAGCAGCAGCTGGTCCCCTG 602
OY	96 LeuAlaLYsArCYshieserApThrgInValPheleuCysSeerleupeuAlaProval 115
Dd	603 CTCAMCAAACTGCCACCGCGCACCCAGAGCTTCCTCTGCTGCTTCGCGCCGCTC 662
OY	116 CysLeuAspArgProleuTYrProCYsArgserleuCysGluAlaValatrgAlaGlyCys 135
Dd	663 TGCCTGACCGGCCCATCTCACCGGTGTGGCTCTGCGAGGCGGAGCGAGCTGTGC 722
OY	136 AlaProleuMetGluAlaTYrGlyPheProTrpProglumetleuHieCysHieLYsPhe 155
Dd	723 GAACCGGTATCATGACTTCTGGGCTTTACTAGCGCCCGAAGTGTTAAGTGTGCAAGTTC 782
OY	156 ProleuAspAsnapleuCysTlleAlaValGlnPheglYHis---LeuProAlaIthrAla 174
Dd	783 CCC---GAGGGGAGCATCTGTGATCCCATGACGCCGCCCATGCCAAGAGCTCCAG 839

OY		175	proProValThrIlyIleCYAlaIeInlCyBgIlmeGluThiAserAlaAspGIylemEC	194
Dd		840	CCCCAAGGCACAAcCGStGTCTCCCTCCTGTATCAACGAGTTGAATCTGAGGCCATCATTT	899
OY		195	GluGlInMeCYsSerSerAspPheValIlylSmetArgIleTyBGilUileLySIleGIu	214
Dd	::::	900	GAACATCTCTGTGGCCAGCGAGTTTGCACCTGAGAGATGAATAATTAAGAAGTGAAAAAGAA	959
OY		215	AenGIyAbPAglyLysLeuIIleGIyAlaGIlnlyBlyBlyBlyBleuLeuLYsPProGIlyPPro	234
Dd	::::	960	AATGGCGCAAGAAAGAAATTGTG-----CCCAAAGAAAGAAAGCCCCTGAAATTGGGGCCC	1013
OY		235	LeuIySAaglyBAspThrIyArghLeuValIleuHsmetLysAenGIyAlaGIlyCyAsPPro	254
Dd	::::	1014	ATCAAGAAAGAAAGAACCTTGAAAGAGTTGTGTGCTGACTCGAAGAAAGTGGSGCTGACTGTCC	1073
OY		255	CysPProGlnLeuAspSerLeuAlaGIlySerPheLeuValImeGIyArgLySValAspGIly	274
Dd		1074	TGCCACCAGCTGGAGACAACCTCACGCCACCACTTCCTCATCACTGGGCGCGCAAGSTGAAGAC	1133
OY		275	GlnLeuLeuLeuMetAlaValTYrArgITrpAspIlyBlyBAenlyBGIImeLYsPheAla	294
Dd	::::	1134	CAGTACTTGCTGACGGCCATCCACACAAAGTGGGACAAGAAAACAAAGAGATTCAAAAACCTTC	1193
OY		295	VallysPheMetPheSerTYrProCySserLeuTYrryrProPhePhe	310
Dd		1194	ATGAAGAAATGAATAAACCATGAGAGTGGCCCCACCTTCACTGCTCGGTGTTT	1241

Search completed: March 23, 2006, 07:03:31
Job time : 698 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 06:59:31 ; Search time 4508 Seconds
(without alignments)
3290.041 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGAGVTRALALLLG.....MPSYPSLYPPFYGAEPH 317

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame.p2n.model -DEV=xlh
-Q=/abes/ABSSWEB_spool/US10768566/runat_22032006_155809_25271/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes04
-USER=US10768566@CSN_1_1_5315@runat_22032006_155809_25271 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: gb_estc1:*
2: gb_estc2:*
3: gb_estc3:*
4: gb_hic:*
5: gb_estc4:*
6: gb_estc5:*
7: gb_estc6:*
8: gb_estc7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1726	89.8	1819	4	CR596705 full-length
2	1421	82.1	1039	1	AY410883
3	1386.5	80.1	1039	1	AL538532
4	1382	79.9	873	10	AY410884
5	1361.5	78.7	799	10	AY410885
6	1335	77.2	819	7	CJ025307
7	1102	63.7	635	7	CK626659

8	1099	63.5	934	5	BX715714	BX715714
9	1096	63.4	934	5	BX719991	BX719991
10	1079.5	62.4	1026	5	BQ879095	BQ879095
11	986	57.0	593	2	BP329572	BP329572
12	959	55.4	566	7	CP982574	CP982574
13	956	55.3	611	6	CD673335	CD673335
14	945	54.6	606	3	BP329610	BP329610
15	910	52.6	657	6	CD518814	CD518814
16	891	51.5	664	5	BY741671	BY741671
17	888	51.3	2704	4	AK088868	AK088868
18	871	50.3	2298	4	AK081052	AK081052
19	860	49.7	1141	8	DN664190	DN664190
20	827	47.8	738	5	BQ771388	BQ771388
21	814	47.1	730	11	CR806571	CR806571
22	808	46.7	562	6	CB609383	CB609383
23	794.5	45.9	610	3	BM490250	BM490250
24	789	45.6	835	6	CF152416	CF152416
25	786.5	45.5	779	6	CB247875	CB247875
26	782.5	45.2	1190	8	DN684942	DN684942
27	751	43.4	441	3	BM716341	BM716341
28	750.5	43.4	713	6	CB525580	CB525580
29	737	42.6	662	2	BB647191	BB647191
30	728	42.1	458	3	BM694123	BM694123
31	723.5	41.8	748	6	CB247054	CB247054
32	716.5	41.4	1330	8	DN684943	DN684943
33	715	41.3	536	10	CG646528	CG646528
34	714	41.3	510	6	CB782544	CB782544
35	713	41.2	709	5	BM847760	BM847760
36	707	40.9	532	1	AM765850	AM765850
37	706	40.8	1011	5	BU196604	BU196604
38	685	39.6	685	6	CF727313	CF727313
39	678.5	39.2	1291	6	CD518463	CD518463
40	673.5	38.9	647	1	AW957689	AW957689
41	657	38.0	664	7	CK686080	CK686080
42	653	37.7	516	5	BX521125	BX521125
43	649	37.5	824	8	CK337082	CK337082
44	647.5	37.4	846	8	CK401961	CK401961
45	646	37.3	1239	8	DN677708	DN677708

ALIGNMENTS

RESULT 1	CR596705	1819 bp	mRNA	linear	HTC 17-APR-2005
LOCUS	CR596705				
DEFINITION	Full-length cDNA clone CSODF024Y06 of Fetal brain of Homo sapiens (human).				
ACCESSION	CR596705				
VERSION	CR596705.1	GI:50477512			
KEYWORDS	HTC; cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Li W.B., Gruber C., Jeejee J. and Polayes D.				
AUTHORS	Full-length cDNA libraries and normalization				
TITLE	Unpublished				
JOURNAL	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600				
REMARK	Paradise Avenue				
REFERENCE	2 (bases 1 to 1819)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				


```

Db      123 TACAAAGCGATGCGGCTGCCCACTGTGAGCAGACGAGAGCGCTGGCCGAGTGAAGCAG 182
Qy      88 GlnAlaSerSerTriLeuProLeuAlaValArgCysHisSerAspThrGlnValPhe 107
Db      183 CAGGCGAGACGCTGGCTGCGCTGCTGCGCCAGCGCTGCGCACTCGGATACGAGGTTCTTC 242
Qy      108 LeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyrProCysArgSerLeu 127
Db      243 CTGTGCTGCTCTTTTCCGCGCCGCTGTCTGACCGGCGCCATCATCCGCGCTGCTGCTG 302
Qy      128 CysGlnAlaValArgAlaGlyCysAlaProLeuMetGlnAlaTyrGlyPheProTyrPro 147
Db      303 TCGAGAGCGGTGGCGCCGCGCTGCGCGCGCTGCTGATGAGAGCCCTTCCCTGGCGCT 362
Qy      148 GluMetLeuHisCysHisIlePheProLeuAspAsnAspLeuCysIleAlaValGlnPhe 167
Db      363 GAGATGCTGCACTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 422
Qy      168 GlyHisLeuProAlaThrAlaProProValThrIleCysAlaGlnCysGluMetGlu 187
Db      423 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 482
Qy      188 HisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAspPheValIleCysMetArg 207
Db      483 CACAGTGTGACGCGCTCATGAGCAGATGTGCTCCAGTGAATTTGTGTCACAAATGCGCG 542
Qy      208 IleValGlnIleIleValIleGluAsnGlyAspArgValLeuIleGlyAlaGlnIleValIle 227
Db      543 ATCAAGAGATCAAGATGAGTGAAGATGGGACCGGAGCTGATGAGACCCAGAAAGAAAG 602
Qy      228 LysLeuLeuLysProGlyProLeuLysArgLysAspThrLysArgLeuValLeuHisMet 247
Db      603 AAGCTGCTCAAGCGCGGCGCCCTGAGAGCCGAGAGACCAAGGCGGTGCTGCTGCAATG 662
Qy      248 LysAsnGlyAlaGlyCysProCysProGlnLeuAspSerIleuAlaGlySerPheLeuVal 267
Db      663 AAGAAATGGCGCGGCGCTGCGCTGCCACAGCTGAGCAGCGCTGGCGGCGAGCTTCTGTC 722
Qy      268 MetGlyArgLysValAspGlyGlnLeuLeuMetAlaValTyrArgTrpAspLysLys 287
Db      723 ATGGCGCGCAAGATGAGTGAAGCAGTGTGCTCATGCGCTCAACCGCTGAGCAAGAG 782
Qy      288 AsnLysGluMetLysPheAlaValIleValPheMetPheSerTyrProCysSerLeuTyr 307
Db      783 AATAGGAGATGAAGTTTGCAGTCAATTCATTTCTTCACTCCCTGCTCCTTACTAC 842
Qy      308 ProPhePheTyrGlyAlaAlaGluProHis 317
Db      843 CTTTCTTCTTACGCGGCGGAGAGCCCGAC 872

RESULT 3
AL538532 1039 bp mRNA linear EST 24-MAR-2004
LOCUS AL538532 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CSDB024YP06 5-PRIME, mRNA sequence.
ACCESSION AL538532 GI:45714242
VERSION AL538532.3
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1039)
REFERENCE
AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
On Feb 13, 2001 this sequence version replaced gi:11261122.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Nott-oligo(dt) primer. Five prime

```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 5245.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna/CSDB024YD030P1&c=5245.r>.

FEATURES

source

```

1..1039
location/Qualifiers
  organism="Homo sapiens"
  mol_type="mRNA"
  db_xref="taxon:9606"
  clone="CSDB024YP06"
  tissue_type="FETAL BRAIN"
  dev_stage="fetal"
  clone_id="Homo sapiens FETAL BRAIN"
  note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Nott-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

```

ORIGIN

Alignment Scores:

```

Pred. No.: 3,44e-130 Length: 1039
Score: 1386.50 Matches: 277
Percent Similarity: 95.84 Conservative: 0
Best Local Similarity: 95.84 Mismatches: 10
Query Match: 80.18 Indels: 7
DB: 1 Gaps: 0

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US-10-768-566-1 (1-317) x AL538532 (1-1039)

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Qy      1 MetArgAlaAlaAlaAlaGlyCysValArgThrAlaAlaLeuLeuLeuGly 20
Db      121 ATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGG 180
Qy      21 AlaLeuHisTrpAlaProAlaArgCysGlu-GluTyrAspTyrTyrGlyTrpGlnAlaGly 40
Db      181 GCGCTGCACTGGCGCGCGCGCGCGCGCGCGCTGAGAGTACACTATGCTGCGAGCGCA 240
Qy      40 UProLeuHisGlyArgSerTyrSerLysProProGlnCysLeuAspIleProAlaAspLe 60
Db      241 GCCGCTGACGCGCGCTCTTACTCAAGCCCGGAGGCTTGACATCTCCCTGCGCACT 300
Qy      60 UProLeuCysHisThrValGlyTyrLysArgMetArg-LeuProAsnLeuLeuGlnHisG 80
Db      301 GCCGCTGCGCACAGGTTGGGCTACAGCGATGCGAGTCCCACTGCTGAGACAG 360
Qy      80 LysSerLeuAlaGlyValLysGlnGlnAlaSerSerTriLeuProLeuAlaValArgC 100
Db      361 AAGGCTGCGCGAGATGAAGCAGCGAGGAGGAGCTGCTGCTGCTGCGCAAGCGCT 420
Qy      100 YHisSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgP 120
Db      421 GCCACTCGGATACGAGAGTCTTCTGTGCTGCTGCTTGGCGCGCTGTCTGACCGCGC 480
Qy      120 TollyrTyrProCysArgSerLeuCysGlnAlaValArgAlaGlyCysAlaProLeuMetC 140
Db      481 CCATCTACCCCGCGCTGCTGCTGCGAGCGCGCTGCGCGCGCGCGCTGCTGCTGCAAG 540
Qy      140 LysAlaTyrGlyPheProTyrProGluMetLeuHisCysHisLysPheProLeuAspAsn 160
Db      541 AAGGCTGACGCTTCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy      160 AspLeuCysIleAlaValGlnPheGlyHisLeuProAlaThrAlaProValThrIle 180
Db      601 ACCTTGATGCGCGTGGAGTTCGGGACCTGCGCGCGCGCGCTCAAGTGAACAGAG 660
Qy      180 LeCysAlaGlnCysGluMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSer 200
Db      661 TCTGCGCCAGTGTGATGAGCAGCAGTGTGAGCGGCTCATGAGAGAGATGTCTCA 720

```

QY	200	etAspPheValValIysMetArgIleValGluIleIleValIleGluAenGIyAspArgIysL	220
Db	721	GTGACTTTGTGTCTCAAAATGCGCATCAAGAGATCAAGATGAGATGCGGACCGGAAGC	780
QY	220	euIIIGIyAlaGlnIlySlySlySlySleuLeuLeuProGIyProleuysArgIysAspT	240
Db	761	TGATTGGAGCC-CAGAAAAGAAAGAGCTGCTCAAGCCGGCCCCCTGAAAGCCCAAGACA	839
QY	240	hLyAsArgIeuValIleuHISMetIysAsenGIyAlaGIyCyAsProCyAsProGlnIleuAsPS	260
Db	840	CCAAAGCGGTGTGTCTGTCACATGAAGAATGGCGGGGCTGCCCC-TGCCACAGCTGACACA	898
QY	260	eFLeuAlIGIySerPheIeuValIMetGIyArgIyValAspGIyGlnIleuLeuMetA	280
Db	899	GGCTGCGGGGSAAGCTTCTCGGTATAGGGCCGMAARTK-GATTGACARCTGCT-CTCATGG	956
QY	280	laValTYrArgITrpAspIlySlyS	287
Db	957	CCKy-TACGCTTGRRMAAAAAA	978
RESULT 4			
LOCUS	AY410884	873 bp	DNA linear GSS 16-DEC-2003
DEFINITION	Pan troglodytes SFRS gene, VIRUTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY410884		
VERSION	AY410884.1	GI:39766852	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Pan.		
AUTHORS	1 (bases 1 to 873)		
	Clark A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Slnsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PubMed	14671302		
REFERENCE	2 (bases 1 to 873)		
AUTHORS	Clark A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Slnsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..873		
	/organism="Pan troglodytes"		
	/mol_type="genomic DNA"		
gene	/db_xref="taxon:9598"		
	<1..>873		
	/gene="SFRS"		
	/locus_tag="HCM4039"		
ORIGIN			
Alignment Scores:			
Pred. No.:	7,61e-130	Length:	873
Score:	1382.00	Matches:	258
Percent Similarity:	89.0%	Conservative:	0
Best Local Similarity:	89.0%	Mismatches:	32
Query Match:	79.9%	Indels:	0
DB:	10	Gaps:	0
QY	US-10-768-566-1 (1-317) * AY410884 (1-873)		
	28 ATGCGAGIUGIUGTyrAspTyrTyrIGIyTrpGlnAGIUGProleuHISGlyArgSerTyr		47

Db	1	CGCTGCGAGGATGCACTACTATGAGGTGGAGGCCAGGCGGTGCACGGCGCTCTTAC	60
QY	48	SerLysProProGlnCysLeuAsp116ProAlaSerLeuProLeuCysSH1stHValGly	67
Db	61	TCCAGGCCGCGCGAGTGCCTTGGAATCCCTGCGACCTGCGCTCTGCCACAGGTGGC	120
QY	68	TyrIAsArgMetArgLeuProAsnLeuLeuGlnH1AsG1SerLeuAlaGluValIysGln	87
Db	121	TACAAGCGCATGCGGCTGCCCACTCTGTGAGACAGAGAGCTGGCCGGAAGTGAACAG	180
QY	88	GlnAlaSerSerTyrPLeuProLeuLeuAlaIysArgCysH1SerAspThrGlnValPhe	107
Db	181	CAGCGAGACAGCTGGCTGCCCTCTGCGCAGGCGCTGCCACTTGAGTACGACGTCTTC	240
QY	108	LeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyrProCysArgSerLeu	127
Db	241	CTGTGCTGCTCTTGTGGCCCGCTGTGTGCACGGCGCCATCTACCCGTGCGTCTG	300
QY	128	CysGlnAlaValArgAlaGlyCysAlaProLeuMetGlnAlaTyrGlyPheProTyrPro	147
Db	301	TGGCAGGCGCGTGGCGCGCGGTGGCGCGGTGATGAGAGGACTACGGCTTCCCTGGC	360
QY	148	GluMetLeuH1sCysH1sLysPhePheProLeuAspAsnAspLeuCysIleAlaValGlnPhe	167
Db	361	NN	420
QY	168	GlyH1sLeuProAlaThrAlaProProValThrIysIleCysAlaGlnCysGluMetGlu	187
Db	421	NN	480
QY	188	H1sSerAlaAspGlyLeuMetGlnGlnMetCysSerSerAspPheValValLysMetArg	207
Db	481	CACAGTGTCTACGGCTCATGATGAGACAGATGTCCTCAGTGACTTGTGTGTCACAAATGCGC	540
QY	208	IleIysGlnIleIysIleGlnAsnGlyAspArgLysLeuIleGlyAlaGlnLysLys	227
Db	541	ATCAAGAGATCAAGATAGAGAAAGAGGAGACCGGAAAGCTGATTTGAGGCCCAAAAGAG	600
QY	228	LysLeuLeuLysProGlyProLeuLysArgLysAspThrLysArgLeuValLeuH1sMet	247
Db	601	AAGCTGCTCAAGCGCGGCGCCCTCTGAAACGCAAGACCAAGACGCGTGGTGGACATG	660
QY	248	LysAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeuVal	267
Db	661	AAGAAAGCGCGCGGCTGCCCTGCCACAGCTGACAGCTGGCGGCGCACCTTCTGTGTC	720
QY	268	MetGlyArgLysValAspGlyGlnLeuLeuLeuMetAlaValIysArgTyrAspLysLys	287
Db	721	ATGGGCGCGCAAGGTGATGACAGCTGCTGCTCATGCGCTTACCCCTGGGCAAGAG	780
QY	288	AsnIysGlnMetLysPheAlaValIysPheMetPheSerTyrProCysSerLeuTyrTyr	307
Db	781	AATAAGAGATGAAGATTGGCGGTCAAAATCATGTTCTTACCCCTGCTCTCTACTAC	840
QY	308	ProPhePheTyrGlyAlaAlaGluProH1s	317
Db	841	CTTTCTTCTTACGGGCGCGCAGAGCCCCAC	870
RESULT 5	AY410885	799 bp DNA linear GSS 16-DEC-2003	
LOCUS	AY410885	Mus musculus SPBP5 gene, VIRIDAL TRANSCRIPT, partial sequence,	
DEFINITION	AY410885	genomic survey sequence.	
ACCESSION	AY410885	GI:39766853	
VERSION	AY410885.1	GI:39766853	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 799)		

AUTHORS	Clark,A.G., GJanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE	2 (bases 1 to 799)			
AUTHORS	Clark,A.G., GJanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
FEATURES	location/Qualifiers			
source	1..799			
gene	/organism="Mus musculus"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:10090"			
	<1..>799			
	/gene="SFRP5"			
	/locus_tag="HMC4039"			
ORIGIN				
Alignment Scores:				
Pred. No.:	8,16e-128	Length:	799	
Score:	1361.50	Matches:	254	
Percent Similarity:	89.3%	Conservative:	5	
Best Similarity:	87.6%	Mismatches:	6	
Query Match:	78.7%	Indels:	26	
DB:	10	Gaps:	1	
US-10-768-566-1 (1-317) x AY410885 (1-799)				
QY	28	ArgCysGlnGluIunTyrAapTyrTyrGlyTyrGlnAlaGluProLeuHisGlyArgSerTyr	47	
DB	3	CGGGCGCAGAGTACGACTTCTGCGTGGCAGGCGCGGTGACCGCGCTCTAC	62	
QY	48	SerTyrProProGlnCysLeuAspIleProAlaAspLeuProLeuCysHisThrValGly	67	
DB	63	TCCAAAGCACCAGAGGCTCTCGACATCCCCGCCGATCTGCGCTCTGCACACGCTGCGC	122	
QY	68	TyrTyrArgMetArgLeuProAsnLeuGluHisGlnSerLeuAlaGluValTyrGln	87	
DB	123	TACAGGCGATGGCGCTGCCAACCTGCTGGAGCAGAGAGCGCTGCGAGGTAAACAG	182	
QY	88	GlnAlaSerSerTyrLeuProLeuLeuAlaTyrArgCysHisSerAspThrGlnValPhe	107	
DB	183	CAGGCAAGCAGCGTGGCTGCGACCTGCTGGCGCAAGCCCTGCCACTGACACCCAGGTCTTC	242	
QY	108	LeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyrProCysArgSerLeu	127	
DB	243	CTGCTCGCTCTTCCTCCGCTCCGCTGCTCGACCGACCACTCACTCCCTGCGCTGCTG	302	
QY	128	CysGlnAlaValAlaArgAlaGlyCysAlaProLeuMetGluAlaTyrGlyPheProTyrPro	147	
DB	303	TGGCAAGCCGTGGCGCCGCGCTGCGCTCGCTCATGAGAGGCGCTTACGGATTCTCCCTTGGCCC	362	
QY	148	GlnMetLeuHisCysHisTyrPheProLeuAspAsnAspLeuCysIleAlaValGlnPhe	167	
DB	363	GAGATGCTGACATG-----	376	
QY	168	GlyHisLeuProAlaThrAlaProProValThrTyrValCysValGlnCysGlnMetGlu	187	
DB	377	-----ACCAAGATCTGGCCCACTGGAGATGGAG	406	
QY	188	HisSerTyrAlaAspGlyLeuMetGluGlnMetCysSerSerAspPheValValTyrMetArg	207	
DB	407	CACAGCGCTGATGCTCTCATGGAACGATGTCCTCAAGTACATTGGTGGTCAAGATCGC	466	

QY	208	llelysglunlelysllegluasnGLYAspArglyseuilegilyaaglnlylysls	227
QY <td>208 <td>llelysglunlelysllegluasnGLYAspArglyseuilegilyaaglnlylysls <td>227</td> </td></td>	208 <td>llelysglunlelysllegluasnGLYAspArglyseuilegilyaaglnlylysls <td>227</td> </td>	llelysglunlelysllegluasnGLYAspArglyseuilegilyaaglnlylysls <td>227</td>	227
Db <td>467 <td>ATTAGAGAGATCAGATAGACACAGGGGACCGAAGCTGATTGGAGCCGAGACAGAGAG</td> <td>526</td> </td>	467 <td>ATTAGAGAGATCAGATAGACACAGGGGACCGAAGCTGATTGGAGCCGAGACAGAGAG</td> <td>526</td>	ATTAGAGAGATCAGATAGACACAGGGGACCGAAGCTGATTGGAGCCGAGACAGAGAG	526
QY <td>228 <td>lysleuLeuylsPProglYProLeuLysArgLysAspThrLysArgLeuValIleuHisMet</td> <td>247</td> </td>	228 <td>lysleuLeuylsPProglYProLeuLysArgLysAspThrLysArgLeuValIleuHisMet</td> <td>247</td>	lysleuLeuylsPProglYProLeuLysArgLysAspThrLysArgLeuValIleuHisMet	247
Db <td>527 <td>AACTGCTCAAGGAGGCCCTTTAAACGCGAGGACCAAGAAAGCTGTCTGTCATATG</td> <td>586</td> </td>	527 <td>AACTGCTCAAGGAGGCCCTTTAAACGCGAGGACCAAGAAAGCTGTCTGTCATATG</td> <td>586</td>	AACTGCTCAAGGAGGCCCTTTAAACGCGAGGACCAAGAAAGCTGTCTGTCATATG	586
QY <td>248 <td>lysasnGLYalaglyCyseProCyseProglIleuLysSerIleuValaglySerPheLeuVal</td> <td>267</td> </td>	248 <td>lysasnGLYalaglyCyseProCyseProglIleuLysSerIleuValaglySerPheLeuVal</td> <td>267</td>	lysasnGLYalaglyCyseProCyseProglIleuLysSerIleuValaglySerPheLeuVal	267
Db <td>587 <td>AAGAACGGGGGACACTCCCTTGCCCAAGTATACAACTGACGCGACACTTCCTGTC</td> <td>646</td> </td>	587 <td>AAGAACGGGGGACACTCCCTTGCCCAAGTATACAACTGACGCGACACTTCCTGTC</td> <td>646</td>	AAGAACGGGGGACACTCCCTTGCCCAAGTATACAACTGACGCGACACTTCCTGTC	646
QY <td>268 <td>MetGlyArgLysValaAspGlyLysIleuLeuMetalaValTyrArgTTPAspLysLys</td> <td>287</td> </td>	268 <td>MetGlyArgLysValaAspGlyLysIleuLeuMetalaValTyrArgTTPAspLysLys</td> <td>287</td>	MetGlyArgLysValaAspGlyLysIleuLeuMetalaValTyrArgTTPAspLysLys	287
Db <td>647 <td>ATGGGCGCCGAAAGTAGAGGAGACACTCTCTCTACGGCCCTTACCCCTGGACAAAGAG</td> <td>706</td> </td>	647 <td>ATGGGCGCCGAAAGTAGAGGAGACACTCTCTCTACGGCCCTTACCCCTGGACAAAGAG</td> <td>706</td>	ATGGGCGCCGAAAGTAGAGGAGACACTCTCTCTACGGCCCTTACCCCTGGACAAAGAG	706
QY <td>288 <td>AsnLysgluMetLysPhealaValLysPheMetPheSerTyrProCyseSerLeuTyrTyr</td> <td>307</td> </td>	288 <td>AsnLysgluMetLysPhealaValLysPheMetPheSerTyrProCyseSerLeuTyrTyr</td> <td>307</td>	AsnLysgluMetLysPhealaValLysPheMetPheSerTyrProCyseSerLeuTyrTyr	307
Db <td>707 <td>AATAAGAGAGATGAGTGTGCAGTCAATTCATGTTCTTCATCCCTGTCCCTACTAC</td> <td>766</td> </td>	707 <td>AATAAGAGAGATGAGTGTGCAGTCAATTCATGTTCTTCATCCCTGTCCCTACTAC</td> <td>766</td>	AATAAGAGAGATGAGTGTGCAGTCAATTCATGTTCTTCATCCCTGTCCCTACTAC	766
QY <td>308 <td>ProPhePheTyrGlyValaIaaglnProHis</td> <td>317</td> </td>	308 <td>ProPhePheTyrGlyValaIaaglnProHis</td> <td>317</td>	ProPhePheTyrGlyValaIaaglnProHis	317
Db <td>767 <td>CCATTTCATATGGGCGAGCTGAACCCAC</td> <td>796</td> </td>	767 <td>CCATTTCATATGGGCGAGCTGAACCCAC</td> <td>796</td>	CCATTTCATATGGGCGAGCTGAACCCAC	796
RESULT 6			
LOCUS	CJ025307	819 bp	mRNA linear EST 22-OCT-2004
DEFINITION	CJ025307 full-length enriched swine cDNA library, adult trachea Sus		
ACCESSION	CJ025307		
VERSION	CJ025307.1	GI:54533893	
KEYWORDS	EST.		
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa		
	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;		
	Sus.		
REFERENCE	1 (bases 1 to 819)		
AUTHORS	Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,		
TITLE	Okumura,N., Hamasina,N. and Awata,T.		
JOURNAL	PEDE (Pig EST Data Explorer): construction of a database for ESTs		
PUBMED	derived from porcine full-length cDNA libraries		
COMMENT	Nucleic Acids Res. 32 (1), D484-D488 (2004)		
	14681463		
	Contact: Hirohide Uenishi		
	Animal Genome Laboratory, Genome Research Department		
	National Institute of Agrobiological Sciences		
	2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan		
	Tel: +81-29-838-8627		
	Fax: +81-29-838-8627		
	Email: huenishi@affrc.go.jp		
	EST project with full-length enriched cDNA libraries carried out in		
	Animal Genome Research Program (Japan) by National Institute of		
	Agrobiological Sciences and STAFF-Institute		
	Single pass sequencing of clones derived from oligo-capped cDNA		
	library		
	Vector sequences were eliminated by RepeatMasker version 2002/07/13		
	and crossmatch version 0.990319		
	Low quality bases were trimmed based on the quality values.		
FEATURES	Location/Qualifiers		
source	1..819		
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	/db_xref="taxon:9823"		
	/clone="TGH01H100038"		
	/tissue_type="trachea"		
	/dev_stage="adult"		
	/clone_lib="full-length enriched swine cDNA library, adult		
	trachea"		
ORIGIN			
alignment Scores:			

Pred. No.: 4,24e-125 Length: 819
 Score: 1335.00 Matches: 245
 Percent Similarity: 96.9% Conservative: 1
 Best Local Similarity: 96.5% Mismatches: 8
 Query Match: 77.2% Indels: 0
 DB: 7 Gaps: 0

US-10-768-566-1 (1-317) x CJ025307 (1-819)

QY 5 AAlaAlaGlyGlyValArgThrAlaAlaLeuAlaLeuLeuGlyValAlaLeuHisTrp 24
 Db 58 GGGGGGGGAGGG 117
 QY 25 AlaProAlaArgCysGluGlyValArgTrpGlyTyrGlyTyrGlnAlaGluProLeuHisGly 44
 Db 118 GCGCCGGGACACGGCCAGGAGTACGACTACTACGGCTGGAGACCCAGCGCTGCACAGG 177
 QY 45 ArgSerTyrSerTyrProProGlnCysLeuAspGlyProAlaAspLeuProLeuCysHis 64
 Db 178 CGCTGGTACTCCAAAGCGCCCGCCAGTGTGACATCCCGCCGACCTGGCCTCTGCAC 237
 QY 65 ThrValGlyTyrIleArgMetArgLeuProAsnLeuLeuGlnHisGluSerLeuAlaGln 84
 Db 238 ACCGTGGGCTACAAAGGCATGGCGCTGCCCAACTCTGGAGCAGAGAGCTGGCGAG 297
 QY 85 ValIleGlnGlnAlaSerSerTyrLeuProLeuLeuAlaIleArgCysHisSerAspThr 104
 Db 298 GTGAAACAGACAGCGAGCTGTGGCTGGCTGGCCAGAGCTTGCCACTCGACACAG 357
 QY 105 GlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyrProCys 124
 Db 358 CAGGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
 QY 125 ArgSerLeuCysGlnAlaValArgAlaGlyCysAlaProLeuMetGlnAlaTyrGlyPhe 144
 Db 418 CGTGGCTATGGAGAGCCGCTGGCGCCGCTGGCGCCCTGCTATGAGAGCGTACGGCTTC 477
 QY 145 ProTyrProGluMetLeuHisCysHisIleValPheProLeuAspAsnAspLeuCysIleAla 164
 Db 478 CCTGGCCAGAGATGCTGCATGCTGCCCAAGTTCCCTCGAGACAAAGCTGCTGCTGCT 537
 QY 165 ValGlnPheGlnHisIleProAlaThrAlaProProValThrIleValIleCysAlaGlnCys 184
 Db 538 GTGCAGTTGGGAGCCTGCGCCGCGCCAGCTCCAGTACCAAGATCTGGCGCCAGTAT 597
 QY 185 GluMetGlnHisSerAlaAspGlyLeuMetGlnGlnMetCysSerSerAspPheValAla 204
 Db 598 GAGATGGAGCATATGCTCCGATGCTCATGAGACATATGTTCCATGACTTCCGTGTC 657
 QY 205 LysMetArgIleIleValGluIleValIleGlnAsnGlyAspArgIleValIleGlyAlaGln 224
 Db 658 AAAATCGGCTCAAGAGATCAAGATAGAGATGGGAGACCGGAACTGATCCGAGCCGAC 717
 QY 225 LysIleValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 244
 Db 718 AAAAAGAAAGAGTGTCTCAAGCCGGGCCCCCTGAAACCGCAAGGAGCTGTGTG 777
 QY 245 LeuHisMetLysAsnGlyAlaGlyCysProCysPProGlnLeu 258
 Db 778 CTGCACATGAAGAACGCTGCCGCTGCCCTGTGCCGACTG 819

RESULT 7
 CK626659 635 bp mRNA linear EST 26-JAN-2004
 LOCUS m124f01.y1 Mouse RPE/choroid, unamplified. ml/mj Mus musculus cDNA
 DEFINITION clone m124f01 5', mRNA sequence.
 ACCESSION CK626659
 VERSION CK626659.1 GI:41347545
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
 1 (bases 1 to 635)
 AUTHORS
 Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J.,
 Buchoff,P., Wistow,G., and Hjelmeland,L.
 TITLE
 JOURNAL
 Unpublished (2004)
 COMMENT
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 24 row: E column: 01
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers

FEATURES

source

1..635
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="m124f01"
 /sex="Male"
 /tissue_type="RPE/choroid"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Mouse RPE/choroid, unamplified: ml/mj"
 /note="Organ: Eye; Vector: pSPoriT; 6ug total RNA was extracted from 200 adult male mouse RPE/choroid. A directionally cloned cDNA library in the pSPoriT vector(life technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor (5'-pgacttacttcttactgctccgagcgccgctc(15-3'). cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:
 Pred. No.: 1.57e-101 Length: 635
 Score: 1102.00 Matches: 202
 Percent Similarity: 97.6% Conservative: 4
 Best Local Similarity: 95.7% Mismatches: 5
 Query Match: 63.7% Indels: 0
 DB: 7 Gaps: 0

US-10-768-566-1 (1-317) x CK626659 (1-635)

QY 84 GluValIleValGlnAlaSerSerTyrLeuProLeuLeuAlaIleArgCysHisSerAsp 103
 Db 2 GAGGTGAAGACAGAGCAAGAGCTGCTGCCACTGCTGGGCCAAAGCTGCCACTCAAGAC 61
 QY 104 ThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyrPro 123
 Db 62 ACCGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
 QY 124 CysArgSerLeuCysGlnAlaValArgAlaGlyCysValaProLeuMetGlnAlaTyrGly 143
 Db 122 TGCCGCTGCTGTGGAGCCGTGGCGCCGCTGGCTGCCATGAGAGCCCTACCGGT 181
 QY 144 PheProTyrProGluMetLeuHisCysHisIleValPheProLeuAspAsnAspLeuCysIle 163
 Db 182 TTCCTTGGCCCGAATGCTGACCTGCACAAAGTTCCTCCCTGAGACAGACCTTGCATC 241
 QY 164 AlaValGlnPheGlnHisIleLeuProAlaThrAlaProProValThrIleCysAlaGln 183
 Db 242 GCGGTGCAAGTTGGGCACTGCTGCCACCGCGCTCCAGATGACCAAGATCTGTGCCAG 301
 QY 184 CysGluMetGlnHisSerAlaAspIleLeuMetGlnGlnMetCysSerSerAspPheVal 203

Db 302 TGTGAGATGAGACACGCGCTGATGCGCTCATGAGAACGATGCTGCCAGTACTTGTG 361
Qy 204 VALLYSMETARGIILEYSGIUILEYSIILEGUAENGIAASPARGLYSLEUILEGIAA 223
Db 362 GTCAAGATGCCGATTAGAGATCAAGATAGCAACGAGGACCGAAGTTGATTGAGACC 421
Qy 224 GINLYSGLYSGLYSLEULEULYSBPROGILYPROLEULYSARGLYASPTHTLYSARGLEU 243
Db 422 CAGAAGAGAAAGAGCTGCTCAAGGACGAGCCCTTAAGCGCAGAGACCAAGAGAGCTG 481
Qy 244 VALLEUHAMETLYASENGIALAGLYCYSPROCYSPROGINLEULASPSERLEUALAGLY 263
Db 482 GTCCGCAATATAGAGAACGCGGCAAGCTGCCCTTGCCCAAGTTAGACCAACCTGACGCGC 541
Qy 264 SERPHELEUVALMETGLYARGLYSVALAEPGLYGINLEULEULEMECALAVALTYRARG 283
Db 542 ACCTTCCTGCTGATGAGCGCGCAAGTAGAGGAGACAGCTGCTCTACGAGCGCTTACCGC 601
Qy 284 TTPAEPGLYSGLYSASNLYSGLUMETLYSPHEAL 294
Db 602 TGGGACAGAGAAATAGAGATGAGATTTGCA 634
RESULT 8
BX15714 934 bp mRNA linear EST 18-NOV-2003
LOCUS BX15714 XGC-cadpole Xenopus tropicalis cDNA clone TTPA040d06 5',
DEFINITION mRNA sequence.
ACCESSION BX15714 GI:38388283
VERSION BX15714.1 GI:38388283
KEYWORDS
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 934)
Cromling, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
COMMENT
Contact: Cromling MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTPA040d06.plkspf
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NciI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NciI at the 3' end.
Vector: pCS107, Site_1: EcoRI, Site_2: NciI
Host: Escherichia coli DH10B.
Location/Qualifiers
1..934
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTPA040d06"
/dev_stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone_1lb="XGC-tadpole"
/note="Vector: pCS107, Site_1: EcoRI, Site_2: NciI, cDNA
was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NciI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Alignment Scores:
Prid. No.: 5,66e-101 Length: 934
Score: 1099.00 Matches: 191
Percent Similarity: 88.2% Conservative: 40

Best Local Similarity: 72.9% Mismatches: 31
Query Match: 5 63.5% Indels: 0
DB: 5 Gaps: 0
US-10-768-566-1 (1-317) x BX15714 (1-934)
Qy 43 HIEGLYARGSERIYRSERYSPROGLINCYSLEUAPLIEPROALAEPLLEUPROLEU 62
Db 11 AACGGACGGTTCCTATTAATAAGATGATCAATGATGATGATGATGATGATGATGATG 70
Qy 63 CYSEHTTRVALIGLYTYRGLYSARGLEULYSLEULEULEULYSLEULEULYSLEULEULYS 82
Db 71 TGCATTAATGTTGGCTATAAATAAATGATGATGATGATGATGATGATGATGATGATGATG 130
Qy 83 ALAAGUVALYSGINGINALASERSETRPLEUPROLEULUALALYASRGYSEHISER 102
Db 131 CCTAGAGGAGAGACAGAACCGACAGCTGGGTGCTCTACTGCGCAAGCGGTGATGCA 190
Qy 103 AEPHTRGINALPHELEUCYSESERLEUPHEALAPROVALCYSELEUAPRGPROILETYR 122
Db 191 GATACCTGACCTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250
Qy 123 PROCYBARGSERLEUCYSGIUALAVALARGALAGLYCYVALAPROLEUMETGLUALAYR 142
Db 251 CCATGCCGCTGCTCATATGAGAGTAGTGCGGAGACAGCTGTGCCCATCTATGAAATCCAT 310
Qy 143 GLYPHEPROTPROGLUMETLEUHIACYSIHSIHSYPHEPROLEUASPSERLEUCYB 162
Db 311 GGTTCCTCTGCGCAGAGATGTTAACTGCAATTAATTCCTCTTGATTAATGATCTGTGC 370
Qy 163 ILEALAVAGINPHEGLYHISLEUPROALATHRALAPROVALTHLYSILECYSLA 182
Db 371 ATCACTGTCAGATTGGCAGCAAAACAAGTCACTCAGCCAGCAGCAGCAAGATTTGCACT 430
Qy 183 GINCYSGIUMETGLUHSERIALASPCILEUMETGLUINMETCYSESESERPHE 202
Db 431 CAGTGTGAATAAGAACAGAACTCGAAACAATGAGGCTGCAACTTGTGCAAGTCACTTT 490
Qy 203 VALVALYSMETARGIILEYSGIUILEYSIILEGUAENGIAASPARGLYSLEUILEG 222
Db 491 GTGTCAGGATGCGCATTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 550
Qy 223 ALAGINLYSGLYSGLYSLEULEULYSBPROGILYPROLEULYSARGLYASPTHTLYSARG 242
Db 551 GCTCAGAGAGAGAAAGAGTCTCTCAAGCAGAGAAAGCTAAAGAGAGAAAGATTCGCAAG 610
Qy 243 LEUVALLEUHAMETLYASENGIALAGLYCYSPROCYSPROGINLEULASPSERLEUAL 262
Db 611 CTGGTTCGTATTAAGAAACGCGGCAAGTTGCCCATGCTCTCAGCTCGAACCACTAAGT 670
Qy 263 GLYSERPHELEUVALMETGLYARGLYSVALAEPGLYGINLEULEULEMECALAVALTYR 282
Db 671 GGAAGCTTCTTATCATGAGCGGCTGTAAGTGAACATTAATCTTCTTCAAGCCATTCAC 730
Qy 283 ARGTPAEPGLYSGLYSASNLYSGLUMETLYSPHEALVALYSPEHEPHESEYRPRO 302
Db 731 AAGTGGACAGAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
Qy 303 CYSESER 304
Db 791 TGTCTCT 796
RESULT 9
BX15991
LOCUS BX15991 934 bp mRNA linear EST 18-NOV-2003
DEFINITION BX15991 XGC-cadpole Xenopus tropicalis cDNA clone TTPA040d07 5',
mRNA sequence.
ACCESSION BX15991 GI:38392732
VERSION BX15991.1 GI:38392732
KEYWORDS
SOURCE EST.
ORGANISM Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 934)
AUTHORS
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE
Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL
Unpublished (2003)
COMMENT
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPOCALIS SEQUENCE ID: TTPA040d07.plksp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NciI cut cDNA was then ligated into pcsi107 with
EcoRI at the 5' end and NciI at the 3' end.
Vector: pcsi107, Site_1: EcoRI, Site_2: NciI
Host: Escherichia coli DH10B.
Location/Qualifiers

FEATURES
source
1..934
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTPA040d07"
/dev_stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone_lib="XGC-tadpole"
/note="Vector: pcsi107, Site_1: EcoRI, Site_2: NciI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NciI cut cDNA was then ligated into pcsi107
with EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Alignment Scores:
Pred. No.: 1,14e-100 Length: 934
Score: 1096.00 Matches: 190
Percent Similarity: 88.2% Conservative: 41
Best Local Similarity: 72.5% Mismatches: 31
Query Match: 63.4% Indels: 0
DB: 5 Gaps: 0

US-10-768-566-1 (1-317) x BX719991 (1-934)

QY 43 HHSGLVARGSERLYSERLYSPROCGINCYSLAUEGLIAPROALAASPLEUPROLEU 62
DB 11 AAGGACGGCTTATACATAATAGATGATCATGACATCCCTTCGGATCTCCATCTC 70
QY 63 CYSHISTHVAIGLYTYRLYSARWELARGLEUPROASMLLEULGIUHSGLUSERLEU 82
DB 71 TGCCATATGTTGGCTATAAATAATGCGATTGCTTAATTGCTGACACAGACACATG 130
QY 83 ALAGLVALVYGLINGLINALASERERTPLAUPROLEULVALVYARGCYSHISER 102
DB 131 CCGTAGGTAACACCAAGCCAGAGCTGGGCTCTACTGCGCAAGGGGTGCATCGA 190
QY 103 AAPTIRGINVALPHELEUCYSESERLEUPHEALAPROVALCYLEUASPARGTROILETYR 122
DB 191 GATACTCAGCTCTCTGCTCCCTTTTGTCTCCATTGCTTGGAAGACCCATTAT 250
QY 123 PROCYBARSERLEUCYGLIUALAVAGLALGLCYVALAPROLEUMECGLUALATYR 142
DB 251 CCATCCCGGTCCTATGCGAGGTAAGTGGCGGACAGCTGGCCCGCTTATGGAATCTTAT 310
QY 143 GLYPHEPTOTTPROGLIUMELUHSYSHSLVSPHEPTOLEUASPARASPLEUCY 162
DB 311 GGTTTCCCTTGGCCAGAGATGTTGAACCTGCAATAATTCCTTGATATGATCTGATGC 370
QY 163 ILEALAVALGINPHEGLYHISLEUPROALATHRALAPROPROVALTHIRLYSILECYVALA 182
DB 371 ATCACTGTGCAATTTGGCGAGCAACAGTCACTGACGCCACAGTGACCAAGATTTGCACT 430

QY 183 GINCYSGLIUMETGLIHSERALASPGLYLEUMETGLIUMETCYSESERASPHE 202
DB 431 CAGTGTAAATAGAACAGAACTCCGAACATGAGGCTGCACTTTGTGCAAGTACTTT 490
QY 203 VALVALVYMECAAGILELYSGLIULILEYSLIEGLUBNGLYASPARGLYSLIEGLY 222
DB 491 GTGCTACGATGCCCATTTAAAGAACTTAAGTTAGATGAGATGAGATCGAAATCTATGCT 550
QY 223 ALAGLNYSLVSLVSLVLEULYSPROGLYPROLEULYSPARGLYSPERTHLYSARG 242
DB 551 GCTCAGAAAGAAAGAAAGTCTCTCAAGACGAGGAACTTAAAGAGAAAGAAATTCGGAAG 610
QY 243 LEUVALLEUHSMECLYSPANGLYVALGLYSPROCYSPROGINLEUASPSERLEUALA 262
DB 611 CTGGTCTGTATATTAAAGAACGCGCAAGTTGCCCATGTCCTCAGCTGACCAACTAAGT 670
QY 263 GLYSEPHLEUVALMETGLYARGLYVALASPGLYGILEUULEULMEUVALVATYR 282
DB 671 GAAAGCTTTCTTATCATGCGCGCTAAGGTGACATTAACCTTCTTACAGCCATCTAC 730
QY 283 ARGTRAPSLYSLVSPANLYSGLIUMELYSPHEALAVALLYSPHEMETPHESERTYRPRO 302
DB 731 AAGTGGGACAAAGAAAGCAAGATATGAGATGACAGATTTCAATGATCTCTATCCA 790
QY 303 CYSEER 304
DB 791 TGCTCT 796

RESULT 10

BO879095
LOCUS
DEFINITION
AGNCOURT 8124145 LUPSKI dorsal root ganglion Homo sapiens cDNA
clone IMAGE:6178182 5', mRNA sequence.
BO879095
ACCESSION
BO879095.1 GI:22271103
VERSION
BO879095.1 GI:22271103
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 1026)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM1357 row: F column: 07
High quality sequence start: 176
High quality sequence stop: 765.

FEATURES

source

1..1026
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6178182"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NciI; Site_2: SalI; cDNA made by oligo-dt priming.
Directionally cloned using the following adaptors:
5'-GACTAGTTCTAGATCGGAGCGGCCCTT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	6,31e-99	Length:	1026
Score:	1079.50	Matches:	212
Percent Similarity:	88.7%	Conservative:	7
Best Local Similarity:	85.8%	Mismatches:	19
Query Match:	62.4%	Indels:	9
DB:	5	Gaps:	5

US-10-768-566-1 (1-317) x BQ879095 (1-1026)

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QY      1 MetATGAlaAlaAlaAlaAlaGlyValATgThAlAlaLeuAlaLeuLeuGly 20
DB      274 ATGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCGG 333
QY      21 AlaLeuHISTPAlaAlaProAlaArgCysGluGlyuTyraSPtyrTyrGlyTTrGAlaGlu 40
DB      334 GCGCTGCACATGCGCGCGCGCGCGCTGCAGAGTACGACTACTATGCTGCGCGCGCG 393
QY      41 ProLeuHISglYArSerSerTySerLySProProGlnCysLeuAspIleProAlaAspLeu 60
DB      394 CCGCTGCACGCGCGCGCTCTACTCTCAACGCGCGCGCGCGCTGCTGCTGCTGCTGCTG 453
QY      61 ProLeuCySHISThryValGlyTyTyTyValArgMetArgLeuProAlaLeuLeuGlnHISglu 80
DB      454 CCGCTGCACACACGCGCGCGCTACAAAGCGCATGCGCGCTGCCAACCTGCGAGCACGAG 513
QY      81 SerLeuAlaGluValAlaGlnGlnAlaSerSerTrrPLeuProLeuLeuAlaLysArgCys 100
DB      514 ACCCTGCAGGAAGTGAAGACAGAGGAGCAGCTGCTGCCCTGCTGCGCGCGCGCTGCG 573
QY      101 HISerAspThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgPro 120
DB      574 CACTCGAGATCGCAAGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633
QY      121 IleTyProCysArgSerLeuCySGluAlaValaArgAlaGlyCysAlaProLeuMetGlu 140
DB      634 ATCTACCGCTGCGCTGCTGCTGCGAGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTG 693
QY      141 AlaTyTrrGlyPheProTrrProGlnMetLeuHISCySHISlyPhePheProLeuAspAsnArg 160
DB      694 GCTACGCGCTTCCCTGCGCTGAGATGCTGCACTGCCAAGATTCCCTCGAGACACAGAC 753
QY      161 LeuCySHISleAlaValGlnPheGlyHISLeuProAlaThrAlaProProValThrLySile 180
DB      754 CTCTGATGCGCGCTGCTGCTGCGAGCCTGCGCGCGCGCGCTGCTGCTGCTGCTGCTG 813
QY      181 CyAlaGlnCysGluMetGlnHISserAlaAspGlyLeuMetGlnGlnMetCysSerSer 200
DB      814 TCGCGCGAGTGGAGATGAGACAGTGTGACGCGCTGATGACAAATGTCCTCCAG 873
QY      201 AspPheVal-ValLySmetArgIleLyS---GluIleLySIIegIuAn---GlyAspA 218
DB      874 GACATTTTGGGCGCAAAATGCGCATCCAGGAGATCCAGATAGAGAAATGGGGAGCC 933
QY      218 IglYLeu---IIegIyAlaGlnLySlySlySlySlySlySlySlySlySlySlySlySly 233
DB      934 GAAAGCTGGATTTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 993
QY      234 --ProLeuLySArgLyS 238
DB      994 GCCCCTGGAGAGCGCG 1010
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RESULT 11
BP329572 593 bp mRNA linear EST 17-SBP-2004
LOCUS BP329572 Sugano cDNA library, rectum Homo sapiens cDNA clone
DEFINITION

RC703796, mRNA sequence.
BP329572
BP329572.1 GI:52258756
EST.
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
15342556

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RC703796"
/issue_type="rectum"
/clone_lib="Sugano cDNA library, rectum"

ORIGIN

Alignment Scores:

Pred. No.:	9,26e-90	Length:	593
Score:	986.00	Matches:	181
Percent Similarity:	99.5%	Conservative:	1
Best Local Similarity:	98.9%	Mismatches:	1
Query Match:	57.0%	Indels:	0
DB:	3	Gaps:	0

US-10-768-566-1 (1-317) x BP329572 (1-593)

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QY      131 ValATGAlaGlyCysAlaProLeuMetGlnAlaTyTrrGlyPheProTrrProGlnMetLeu 150
DB      44 CTCCGCGCGCGCTGCGCGCGCTCATGAGGCTTACGCGCTTCCCTGCGCGAGATGCTG 103
QY      151 HISCySHISlyPhePheProLeuAspAspLeuCySHISleAlaValGlnPheGlyHISleu 170
DB      104 CACTGCAACAAGTTCCTCCCTGACACGACCTTGCATGCGCGTGCAGATTGGGCACTG 163
QY      171 ProAlaThrAlaProProValThrLySIIegCysAlaGlnCysGluMetGlnHISserAla 190
DB      164 CCGCGCACGCGCGCTTCCAGTACCAAGATCTGCGCGCGCGCTGATGAGACAGAGTCT 223
QY      191 AspGlyLeuMetGlnGlnMetCysSerSerAspPheValValLySmetArgIleLySglu 210
DB      224 GACGCGCTCATGAGCAATGATGCTCCAGTACTTGGTCAAAATGCGCATCAAGAG 283
QY      211 IleLySIIegIuAnGlyAspArgLySleuIIegIyAlaGlnLySlySlySlySlySlySly 230
DB      284 ATCAAGATAGGAATGGGAGACGGAAGCTGATGGAGCCGAAAGAAAGAAAGAGCTGTC 343
QY      231 LysPProGlyProLeuLySArgLySAspThrLySArgLySValLySmetLySAsnGly 250
DB      344 AAGCGGCGCGCGCTTGAACGCAAGACACCAAGCGCGCTGCTGCTGCTGCTGCTGCTG 403
QY      251 AlaGlyCyProCyProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArg 270
DB      404 GCGGCGCTGCCCTGCGCACAGCTGGAAGCTGCGGGGAGCACTTCTGCTGATGGGCGCG 463
QY      271 LysValaAspGlyGlnLeuLeuMetAlaValTyTrrATGTrpAspLySlySlySlySly 290
DB      464 AAGGATGAGACAGAGTCTGCTCATGGCGCTTACCGCTGCGACAAAGAAATTAAGAG 523
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Qy	291	Methylphenylaminalvalylphenylphenylserine	ProCysSerLeuTyrTyrProPhe	310
Db	524	ATGAAGTTGCAGTCATTCATGTTCTCTACCCCTCTCTCTACTACCTTCCTTC		583
Qy	311	TyrGlyAla	313	
Db	584	TACGGGCGC	592	
RESULT 12				
LOCUS	CP982574	566 bp	mRNA	linear
DEFINITION	ma165906.v1 McCarrey Eddy 18 day preleptotene spermatocytes Mus			EST 18-DEC-2003
VERSION	musculus cDNA IMAGE:7030808 5' similar to TR:Q9WU66 Q9WU66			
KEYWORDS	SECRETED FRIZZLED-RELATED PROTEIN 5. ; mRNA sequence.			
ACCESSION	CP982574			
VERSION	CP982574.1	GI:38515623		
KEYWORDS	EST.			
SOURCE	Mus musculus			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 566) McCarrey,J., Eddy,M., Marz,M., Hillier,L., Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Bowery,Y., Theising,B., Gibbons,M., Ritter,E., Tagareishvili,R., Ronko,I., Maguire,L., Kennedy,S., Bennett,J., Waterston,R. and Wilson,R.			
TITLE	NIHNS Mouse			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: McCarrey/Eddy NIHNS Mouse NIHNS Mouse Washington University School of Medicine 444 Forest Park Parkway, Box 850L, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics) - excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Seq primer: Primer name ambiguous. Location/Qualifiers 1..566 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:7030808" /sex="male" /tissue_type="18-day preleptotene spermatocytes" /lab_host="DH10B (phage-resistant)" /clone_idb="McCarrey Eddy 18 day preleptotene spermatocytes" /note="Organ: testis; Vector: pBluescript SK+ (Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo dT-primed [5'-(GA)10-ACTAGTCCTCAGTTTCTTTT-3'] and directionally cloned using 5' linkers 5'-AATTCGCACGAG-3' and 5'-CTCGTCGC-3'. Size selection of >400bp material gives average insert size ranging from 1.2 kb. Library was mass excised (from lambda-Unizap-XR) and resulting single-stranded phagmids were prepaped and transformed into DH10B. Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences)."			
ORIGIN				
Alignment Scores:				
Pred. No.:	4,86e-87	Length:	566	
Score:	959.00	Matches:	179	
Percent Similarity:	96.8%	Conservative:	6	
Best Local Similarity:	94.7%	Mismatches:	4	
Query Match:	55.4%	Indels:	1	

DB:	7	Gaps:	0
US-10-768-566-1 (1-317) x CP982574 (1-566)			
QY	104	ThisInvalPheueuCySserIeuPheuaIaProvaIcySeIeuAaPaArgProIleTyPro	123
Db	1	ACCCAGAGCTTTCCTCTGCTCGCTCTTGCTCCCTGCTGACCGACCCATCTAACCCC	60
QY	124	CyAaRgsereIeuCySgluaIaValArgAlaGlyCySaIaProIuMeuGluAlaTyTcyI	143
Db	61	TGCGGCTCGCTGCGGAAGCGTGGCGGCGCGCTGCGCTTCACAGAGAGCTTAACGCT	120
QY	144	PheProTrpProGluMeuIeUhiSaCyAhiSlySaPheProIeuAaPaAspIeuCySile	163
Db	121	TTCCCTTGCGCCGAGATCTGCACTGCCACAAAGTCCCCCTGGACAAAGACTCTGCATC	180
QY	164	AlaValaInPhegluYhiSleuProaIaThraIaProProVaIThrySileCySaIaGln	183
Db	181	GGCGTGCAAGTTCCGGGCACTGCTCCGCCACCGCGCTCAAGTGAACAAAGATCTGAGCCAG	240
QY	184	CySgluMeuGluhiSserIaIaPegIyIleuMeuGluGluMeuCySserSeraPheVal	203
Db	241	TGTAAGATGGAGCAACGCTGAAGGCTCAATGAAACAGAGTGTCTCAGAGACTTGTG	300
QY	204	ValIlySmeIaRglIeIySgluIleIySilegluSangIyAsPaRgIySleuIeGlyAla	223
Db	301	GTCAAGATGCCCATTAAGAGATTAAGATAGACAAACGGGACCCAAAGTTATTTGAGCC	360
QY	224	GluIySlySlySlySleuIeuIyProGlyProIeuIySargIySaPThrySaRglu	243
Db	361	CAGAAAGAAAGAAAGCTGCTCAAGCAAGGCCCCCTTAAGCGCAAGACCAAGAAAGCTG	420
QY	244	ValIeuhiSmeIySaNgIyAlaGlyCyAProCySProGluIeuAaPserIeuAlaGly	263
Db	421	GTCTCGATTTGAAAGAACGGGCGAAAGCTGCTTGTCCACAGTTAGCAACCTACGGGC	480
QY	264	SerPheIeuIyMeuGlyARgIyValaIaSpGlyGluIeuIeuIeuMeuAlaValTyArg	283
Db	481	AGCTTCTGTGATGGCGCGCAAGTGAAGGAGACAGCTGCTTCACGGCGCTTACCGC	540
QY	284	TrPaSPlYslySaenIySgluMeIyS	292
Db	541	TGGGACAAAGAA-ATAAGAGATGAAG	566
RESULT 13			
CD673335			
LOCUS	611 bp	mRNA	linear
DEFINITION	fg3g92.y1 Human Iris cDNA (Normalized) : fg Homo sapiens cDNA clone		
ACCESSION	CD673335		
VERSION	CD673335.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 611)		
AUTHORS	Wiatcow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.		
TITLE	Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium		
JOURNAL	Mol. Vis. 8 (4), 185-195 (2002)		
PUBMED	12107412		
COMMENT	Contact: Wiatow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 23 row: 9 column: 02		

Qy	271	LYSVALAPGGLYGINTLEULEUUEWELALVALTYRATGTPAPPLYSLYSANLYGCU	290
Db	464	AAAGCGATGACCACTGCTGCTCATGGCCGGCTACCGCTGGCAGACAGAGATAGAGAG	523
Qy	291	MELTYPHPHEALAVALLYPHEWEPHESERTYRPROCYSERLEUTYRTPROPHE-PH	310
Db	524	ATGAAGCTTGGAGTCATCATGTTCTTCCTACCCCTGCTCCTTACTACCTTTCCCT	583
Qy	310	ETYRGLYALA-ALAGIUDPROHIS	317
Db	584	TACGGGCGCGGACAGCCGCCAC	606
RESULT 15			
LOCUS	CD518814		
DEFINITION	AGENCOURT 14375702 NIH MGC 181 Homo sapiens CDNA clone	957 bp	mRNA linear EST 06-JUN-2003
ACCESSION	CD518814		
VERSION	CD518814.1	GI:31450532	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 957)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Daniela S. Gerhard, Ph.D.		

CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAW492 row: 1 column: 03
High quality sequence step: 488.

FEATURES

SOURCE

1. .957

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3040886"
/cisue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH08-Ton A (T1 and T5 phage resistance)"
/clone_1ib="NIH_MGC_181"
/notes="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
(destroyed); library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
[Invitrogen]. Note: this is a NIH_MGC library."

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ORIGIN

Alignment Scores:

Pred. No.:	1,05e-81	length:	957
Score:	910.00	Matches:	170
Percent Similarity:	89.6%	Conservative:	3
Best Local Similarity:	88.1%	Mismatches:	11
Query Match:	52.6%	Indels:	9
DB:	6	Gaps:	1

US-10-768-566-1 (1-317) X CD518814 (1-957)

QY 1 MetcAGAlaAlaAlaAlaAGIyGlyValaArgThraAlaAlaAlaAlaLeuLeuLeuGly 20
DB 100 ATGCGGGCGGGCGGGCGGGCGGGCGGTGCGGACGGCGCGCGTGGCGCTGCTGCTGGGG 150

Qy	21	AlALeuNI:ETPAlAeProlAlaRySgVnGluYrAaBYrYrYGLYTPGAlaIaGlu	40
Db	160	GGCCTGCACTGGCGCGCGCGCTGCAGAGAGTACACTATGCTGGCGAGCGCGAG	21.9
Qy	41	ProLeuNIhGILyArSgETrYsETrYsPrOPrOGInCYsLeuAaPrlIeProlAaPLeu	60
Db	220	CCCTGTCAGCGCGCGCTCTACTCCAAAGCGCGCGCACTGTGACATCCCTGGCCGACTTG	27.9
Qy	61	ProLeuCYaNIeThrValGILYrYrYrYbArMeCaRgLeuProAnLeuLeuGILNIhGILu	80
Db	280	CCGCTCTGGCACAAGGTGGGCTACAAAGGCATCGCGCTGCCAACCTGTGGAGACAGAG	33.9
Qy	81	SeTLeuAlaGILyValIySgInGILNIaSeSgETrPLeuProLeuLeuAlaLybArGYs	100
Db	340	AGCCTGGCGGAAGTGAAGACAGACGCGAGCAAGCTGGCTGGCGCTGGCCAAAGCTGCG	39.9
Qy	101	HisSerAPrThGILyValPheLeuCySgETrLeuPheAlaP-roValCYsLeuAaPArPrO	120
Db	400	CACCTGGAATACGAGAGTCTTCTGTGCTCGCTCTTGGCGCGCGTGTGTGTGACCGGCC	45.9
Qy	121	ILeTrProCYaArSgETrLeuCYsGILNIaValArGILaGILyCYbAlaProLeuMeGILu	140
Db	460	ATCTACCCGAGCGGCTCGCTGTGCGAGGCGCGGCGCGCGCTGCGCGCGCTCATGGAG	51.9
Qy	141	AlATrYcGILyPhePrOTrPrProGILuMetLeuNIhCYsYhIlySlys-PheProLeuAaPArAa	160
Db	520	GCTTACCGGCTCCCGCTGAGTGAATGCGGACCTGCACAAAGTTTCCCTCGAGCAACGAG	57.9
Qy	160	pLeuCYbILeAlaValGILNIhPheGILY-----HisLeuProAl	172
Db	580	CGTCTGACATCGCGGTGCAGATTGCGGGAGACTGACCCTGACCGCGAGCTGAGTTGACCA	63.9
Qy	172	aThrAlaPArPrOValThrYsILeCYaAlaGILNIyS	184
Db	640	GATTTGCGCCCGAGGTGTGAAGTGAAGCAACCTTTGC	676

Search completed: March 23, 2006, 08:19:42
Job time : 4515 secs

GenCore version 5.1.7
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OW protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 07:05:30 ; Search time 904 Seconds
(without alignments)
2899.771 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGGCTAATLALILG.....MFSYPCSLYPFYGAAPH 317

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abse/ABSSWB_Spool/US10768566/runat_22032006_155813_25385/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastcap -SUFFIX=p2n.rmpbm
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-HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abse02h
-USER=US10768566@CGN_1_1_1026@runat_22032006_155813_25385 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_Main:*

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10:	/cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1730	100.0	954	6	US-10-338-604-3 Sequence 3, Appli
2	1730	100.0	1905	8	US-10-338-604-1 Sequence 1, Appli
3	1730	100.0	1905	8	US-10-768-566-2 Sequence 2, Appli
4	1730	100.0	1984	5	US-10-146-474-5 Sequence 5, Appli
5	1730	100.0	1984	7	US-10-301-764-5 Sequence 5, Appli
6	1613	93.2	945	6	US-10-338-604-6 Sequence 6, Appli
7	1613	93.2	1186	6	US-10-338-604-4 Sequence 4, Appli

8	924.5	53.4	1308	5	US-10-146-474-18 Sequence 18, Appli
9	924.5	53.4	1308	7	US-10-301-764-18 Sequence 18, Appli
10	924.5	53.4	2078	6	US-10-138-434A-1 Sequence 1, Appli
11	924.5	53.4	2094	9	US-10-756-149-3306 Sequence 3306, Ap
12	924.5	53.4	2602	7	US-10-666-851-1 Sequence 1, Appli
13	924.5	53.4	4500	6	US-10-138-434A-27 Sequence 27, Appli
14	917	53.0	942	6	US-10-425-586-2 Sequence 2, Appli
15	917	53.0	942	7	US-10-466-136-2 Sequence 2, Appli
16	917	53.0	1017	6	US-10-425-586-9 Sequence 9, Appli
17	916	52.9	2075	6	US-10-138-434A-2 Sequence 2, Appli
18	916	52.9	2075	7	US-10-425-586-1 Sequence 1, Appli
19	916	52.9	2075	7	US-10-466-136-1 Sequence 1, Appli
20	916	52.9	4462	3	US-09-974-298-28 Sequence 28, Appli
21	916	52.9	4469	3	US-09-796-008-1 Sequence 1, Appli
22	916	52.9	4469	6	US-10-133-937-42 Sequence 42, Appli
23	916	52.9	4469	6	US-10-172-118-857 Sequence 857, App
24	916	52.9	4469	7	US-10-159-563-42 Sequence 42, Appli
25	916	52.9	4469	7	US-10-342-887-857 Sequence 857, App
26	916	52.9	4469	8	US-10-786-720-15 Sequence 15, Appli
27	916	52.9	4469	8	US-10-788-792-21 Sequence 21, Appli
28	916	52.9	4469	8	US-10-473-974-203 Sequence 203, App
29	916	52.9	4469	8	US-10-817-525-1 Sequence 1, Appli
30	714	41.3	804	6	US-10-425-586-12 Sequence 12, Appli
31	659	38.1	741	6	US-10-425-586-11 Sequence 11, Appli
32	625	36.1	885	3	US-09-934-483A-2 Sequence 2, Appli
33	625	36.1	1799	3	US-09-934-483A-4 Sequence 4, Appli
34	625	36.1	1859	3	US-09-934-483A-3 Sequence 3, Appli
35	625	36.1	2030	5	US-10-146-474-1 Sequence 1, Appli
36	625	36.1	2030	7	US-10-301-764-1 Sequence 1, Appli
37	624	36.1	1380	8	US-10-783-528-49 Sequence 49, Appli
38	624	36.1	1382	6	US-10-295-027-1128 Sequence 1128, Ap
39	624	36.1	1988	6	US-10-473-974-197 Sequence 197, App
40	624	36.1	1988	6	US-10-177-293-141 Sequence 141, App
41	624	36.1	2027	2	US-08-949-904-1 Sequence 1, Appli
42	621.5	35.9	2379	4	US-09-925-065A-678403 Sequence 678403, Ap
43	620	35.8	2085	5	US-10-106-698-2105 Sequence 2105, Ap
44	616	35.6	1869	3	US-09-981-876-56 Sequence 56, Appli
45	616	35.6	1869	3	US-09-148-545-56 Sequence 56, Appli

ALIGNMENTS

RESULT 1
US-10-338-604-3
; Sequence 3, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; FILE REFERENCE: MP101-250PIRM
; CURRENT APPLICATION NUMBER: US/10/338, 604
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-338-604-3

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Pred. No.: 2.04e-205
Score: 1730.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 6
Gaps: 0

US-10-768-566-1 (1-317) x US-10-338-604-3 (1-954)

Qy	241	YysarTgIueValIleuHISMerLySaBnGlyIaAGIYCySPROCYsProGlnLeuAspSer	260
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Qy	261	LeuIaGIsYserPheLeuValMetGlyIaTgLySValAspGlyGlnLeuLeuMetAla	280
Db	962	CTGGCGGGCAGCTTCTCTGTGTATGGGCGGCAAGTGGATGGACAGCTGTGTCAATGGCC	1021
Qy	281	ValIYrArGtTPAsPlyLySaAnLySGLuMetLySpheAlaValIySPheMetPheSer	300
Db	1022	GTCTACCCCTGGGACAAAGAGATAGAGAGAAAGTTGGCAATTCATGTTCTCC	1081
Qy	301	TyrProCYsSerIeutyTyrTyrProPhePheTyrGlyAlaAlaGluProHis	317
Db	1082	TACCCCTGCTCCTCTACTACCTTTCTTCTAAGAGGGCGGCGAGCCCCAC	1132

RESULT 3
US-10-768-566-2

Sequence 2, Application US/10768566
Publication No. US20040259789A1

GENERAL INFORMATION:
APPLICANT: Chada, Kiran K.
APPLICANT: Chouinard, Roland
APPLICANT: Ashar, Hena
APPLICANT: Sayed, Abu
TITLE OF INVENTION: A METHOD OF TREATING OBESITY AND METABOLIC DISORDERS
TITLE OF INVENTION: ADIPOSE TISSUE BY ADMINISTRATION OF sFRP-5 PEPTIDE
FILE REFERENCE: 69014-B
CURRENT APPLICATION NUMBER: US/10/768,566
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1905
TYPE: DNA
ORGANISM: Human
US-10-768-566-2

[illegible]

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1      RESULT 4
2      US-10-146-474-5
3      ; Sequence 5, Application US/10146474
4      ; Publication No. US20030023061A1
5      ;
6      GENERAL INFORMATION:
7      APPLICANT: Umaneky, Samuil
8      Melkonyan, Hovsep
9      TITLE OF INVENTION: A FAMILY OF GENES ENCODING
10     APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
11     METHODS OF USE THEREOF
12
13     NUMBER OF SEQUENCES: 19
14     CORRESPONDENCE ADDRESSES:
15     ADDRESSEE: MORRISON & FOERSTER
16     STREET: 755 Page Mill Road
17     CITY: Palo Alto
18     STATE: CA
19     COUNTRY: USA
20     ZIP: 94304-1018
21
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS
26     SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28     CURRENT APPLICATION DATA:
29     APPLICATION NUMBER: US/10/146,474
30     FILING DATE: 14-May-2002
31
32     CLASSIFICATION: <Unknown>
33
34     PRIOR APPLICATION DATA:
35     APPLICATION NUMBER: US/08/937,067
36     FILING DATE: <Unknown>
37
38     ATTORNEY/AGENT INFORMATION:
39     NAME: lehnhardt, Susan K.
40
41     REGISTRATION NUMBER: 33,943
42
43     REFERENCE/DOCKET NUMBER: 23647-20018.00

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 216..1166
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-146-474-5

Alignment Scores:
Pred. No.: 5,79e-205 Length: 1984
Score: 1730.00 Matches: 317
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-768-566-1 (1-317) x US-10-146-474-5 (1-1984)

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DB 216 ATGG 275
QY 21 Alaleuhlstrpalaprolaaagcyaglugluyrabytyrtygltyrptglnaaglu 40
DB 276 GCGCTGCACCTGGGCGCGCGCGCTGCAGAGTACGACTACTATGCTGGGCGGCGAG 335
QY 41 Proleuhalaglyarsetyrtserlyrpprologincyaleuaprilaprolaaapleu 60
DB 336 CCGCTGCACGGGGCTCTCTACTCAAGCCGGCGAGTGTGACATCCCTGCGACCTG 395
QY 61 Proleucyahlstrvalgltyrlyrsarwmetargyleuproaaleuuleugluhlaglu 80
DB 396 CCGCTGCACGAGCGGTGGCTCAACAGCCGATGGCGCTGCCAAGCTGCTGAGCAGAG 455
QY 81 Serleuualaglyvalaglynglnalasersttpleuoproleuualalyahargcy 100
DB 456 AGCCTGGCGGAAGTGAAGCAGCAGCGAGCACTGCTGCGCTGCGCTGCGCAAGCGCTGC 515
QY 101 Hlsseraprrhrglnvalphleucysserleuphealaprovalcyaleuaprrpro 120
DB 516 CACTCGAATACGAGATCTTCTGTGCTGCTGCTTGGCGCGCTGTGCTGCTGCGCGCGCC 575
QY 121 Iletyrprocyarserserleucyaglnuavalargalaglycyaalaproleumetglu 140
DB 576 ATCTACCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635
QY 141 Alatyrglypheprotrproglumetleuhsywhslsyphaproleuaprraprrap 160
DB 636 GCTTACGGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695
QY 161 Leucysilleaavalaglnphelgylhslenprocalatrralaproprovalthiryslle 180
DB 696 CTCTGCATGCGCGTTCAGTTCGGGCACTGCGCGCGCGCGCGCGCTGCCAGTGCACAGATC 755
QY 181 Cysalaglncyaglnumetgluhlseseralaaepglyleumetgluulinmetcyserser 200
DB 756 TGGCGCCAGTGTGAATGAGACAGTGTGACGGCTCATATGAGCAATGTGCTCCACT 815
QY 201 Aapphevalvallymetargilleuysglnllysllegluanglyasparglylsleu 220
DB 816 GACTTTGGTGTCAAAATGCGCATCAAGAGATCAAGATGAGAAATGGGGACCGAAGCTG 875
QY 221 Ileglyalaglnly 240
DB 876 ATTGAGCCCAAGAAAAGAAAGAAAGTGTCTCAAGCGCGCGCGCGCTTGAAGCGCAAGACAC 935

QY 241 Lysargleuvalleuhsimetylalaglycyapprocypprogluleuaprrser 260
DB 936 AAGCGGCTGTGCTGCACATGAAGATGGCGGGGCTGCCCTGCCACAGCTGGACAGC 995
QY 261 Leuhalaglyserpheleuvalmetglyargyvalaprrglyntleuuleuwerla 280
DB 996 CTGGCGGCGACCTTCCTGCTCATGCGCGCAAGTGAATGAGACAGTGTCTCATGAGCC 1055
QY 281 Valtyratgtppaplylasyasnlysglnumetlysphealaavalysphemecpneser 300
DB 1056 GTCTACCGCTGGGACAGAAATGAGAGATGAAGTTGCAAGTCAATTATGATGTCTCC 1115
QY 301 Tyrprocysserleuyltyrtyrpprohephtyrglyalalagluuprrhls 317
DB 1116 TACCCCTGCTCCTCTACTACCTTTCTTACAGGGGCGGCGAGGCCAC 1166

RESULT 5
US-10-301-764-5
Sequence 5, Application US/10301764
Publication No. US20040039184A1
GENERAL INFORMATION:
APPLICANT: Umaneky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & ROEBSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-No. US20040039184A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018, 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 216..1166
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-301-764-5

Alignment Scores:
Pred. No.: 5,79e-205 Length: 1984
Score: 1730.00 Matches: 317
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0


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QY 247 MetLySaenGIyAlaGIyCySeProCySPProGInLeuAspSerLeuAlaGIySerPheLeu 266
DB 730 ATGAAGAAAGGGGCAAGCTGCTTGTCCACATTGACCACTGACGGGAGCTTCTCG 789
QY 267 ValMetGIyArGIyValAspGIyGInLeuLeuMetAlaValTyTrpTrpAspLyS 286
DB 790 GTCATGGGGCGGCAAGTAGAGGACAGCTGTCTACGGCGCTTACCGCTGGAGCAAG 849
QY 287 LysAsnLySGIuMetLySAspPheAlaValLySPhMetPheSerTyProCySAspLeuTy 306
DB 850 AAGATTAAAGAGATGAAGTTTGCGGTCAATTCTTCTCTATCTCTCTCTCTCTAC 909
QY 307 TyProPhePheTyGIyAlaAlaGIuProHis 317
DB 910 TACCTTTTCTATGGGCGAGCTGAACCCAC 942

RESULT 7
US-10-338-604-4
; Sequence 4, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; TITLE OF INVENTION: DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MP101-250P1RM
; CURRENT APPLICATION NUMBER: US/10/338,604
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (242) ... (1186)
US-10-338-604-4

Alignment Scores:
Pred. No.: 1,166-190 Length: 1186
Score: 1613.00 Matches: 295
Percent Similarity: 96.5% Conservative: 5
Best Local Similarity: 94.9% Mismatches: 11
Query Match: 93.2% Indels: 0
DB: Gaps: 0

US-10-768-566-1 (1-317) x US-10-338-604-4 (1-1186)
QY 7 AlaGIyGIyValArGThrAlaAlaLeuAlaLeuLeuGIyAlaLeuHISrTrpAlaPro 26
DB 251 GCTTGAGGCGCACGAGCGGCGGCACTGGCGTGTCTGCTGGGGCGCTGCATGGGCGCA 310
QY 27 AlaArgCySGIuGIyTrpAspTyTrpGIyTrpGInAlaGIuProLeuHISGIyArGSer 46
DB 311 ACAAGCGGCGCAGAGTAGACATACATCGGTTGGCAGCGGCGGCTGACGGCGCTCC 370
QY 47 TySerLySProProGInCySLeuAspLIEProAlaAspLeuProLeuCySHISrTrVal 66
DB 371 TACTCCAAAGCCACCGAGTGCCTCGACATCCCGCGGATCTCGCTGTGTACACGGTGC 430
QY 67 GIyTyTrpLySArGMetArGIuProAsnLeuLeuGIuHISGIuSerLeuAlaGIuValLyS 86
DB 431 GGCTACAAAGCGCATGGGCTGCCAACCTGTGTGAGACAGAGAGCTGGCCAGGTGAAG 490
QY 87 GInGInAlaSerSerTrpLeuProLeuLeuAlaLySArGYSHISerAspTrpGInVal 106
DB 491 CAGGAGGCAAGCAGCTGGCTGCCACCTGCGCCAAAGCGCTGCCACCTCAACACCCAGGTC 550
QY 107 PheLeuCySAspLeuPheAlaProValCySLeuAspArGProLIETyProCyAspArGSer 126
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DB 551 TTCCTGTGCTGCTTCTTGTCCCTCGCTGCTGACCGACCCATCTTACCCTGCCGCTCG 610
QY 127 LeuCySGIuAlaValArGIyGIyCySAlaProLeuMetGIuAlaTyGIyPheProTrp 146
DB 611 CTGTGCAAGAGTGGCGGCGGCGGCTGCGCTCGGCTCATGAGGCTTACGGTTTCCCTTGG 670
QY 147 ProGInMetLeuHISCySHISLySAspPheProLeuAspAsnAspLeuCySIIeAlaValGIn 166
DB 671 CCCGAGAGTGTGCATCGCACACAAAGTTCCCTGTGACAAAGACCTCTGATGCGGTGAG 730
QY 167 PheGIyHISLeuProAlaThrAlaProProValThryLySIIeCySAlaGInCySGIuMet 186
DB 731 TTGGGACCTGTGCTGCCACCGCGCTCATGACCAAGATCTGTGCCAGTGTAGATG 790
QY 187 GIuHISerAlaAspGIyLeuMetGIuInMetCySAspSerAspPheValValLySAsp 206
DB 791 GAGCACAGCGGCTGAGCGGCTCATGGAACAGATGTCTCATGATCTTGTGTGTAAGATG 850
QY 207 ArGIleLySGIuIIeLySIIeGIuAsnGIyAspArGIySLeuIIeGIyAlaGInLySAsp 226
DB 851 CGCATTTAAGAGATCAAGATAGACAAACGGGACCGAAAGTTGATTGAGGCCAGAAAG 910
QY 227 LysLySLeuLeuLySProGIyProLeuLySArGIyAspTrpLySArGIyValLeuHIS 246
DB 911 AAGAGCTGTCTCAAGCGAGCGCCCTTAAGGCGCAAGACCAACAAAGCTGTCTGCAT 970
QY 247 MetLySaenGIyAlaGIyCySeProCySPProGInLeuAspSerLeuAlaGIySerPheLeu 266
DB 971 ATGAAGAAAGGGGCAAGCTGCTTGTCCACATTTAGCAACCTGACGGGAGCTTCTCG 1030
QY 267 ValMetGIyArGIyValAspGIyGInLeuLeuLeuMetAlaValTyTrpTrpAspLyS 286
DB 1031 GTCATGGGCGGCAAGTAGAGGACAGCTGTCTCACGGCGTCTACCGCTGGAGCAAG 1090
QY 287 LysAsnLySGIuMetLySAspPheAlaValLySPhMetPheSerTyProCySAspLeuTy 306
DB 1091 AAGATTAAAGAGATGAAGTTTGCGGTCAATTCTTCTATCTCTCTCTCTCTAC 1150
QY 307 TyProPhePheTyGIyAlaAlaGIuProHis 317
DB 1151 TACCTTTTCTATGGGCGAGCTGAACCCAC 1183

RESULT 8
US-10-146-474-18
; Sequence 18, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Umaneky, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
```

NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33, 943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-146-474-18

Alignment Scores:
Pred. No.: 1.44e-104 Length: 1308
Score: 924.50 Matches: 179
Percent Similarity: 72.8% Conservative: 51
Best Local Similarity: 56.6% Mismatch: 77
Query Match: 53.4% Indels: 9
Gaps: 6

US-10-768-566-1 (1-317) x US-10-146-474-18 (1-1308)

QY	1	Mecargalaaalaaalaaalaglyvalargthralaaaleualauleu-----	18
Db	302	ATGGGCATCGGGCGGACGAGGGGGCGCGCGGGGACGCCCTGGCGTCTGGCG	361
QY	19	leuglialaleuhitrlalprolaargcysglugluytrapytyrtyclttrgln	38
Db	362	CTGGCGCGCGGCTTCTGGCGGTGGGCTCGGCCAGCGATACGATACGTGACCTTCAG	421
QY	39	Alaagu-----Proleuhis---glyrsertryserlyrproglincysleuasp	55
Db	422	TGCGACATCGGCGCCCTTACAGAGCGGGCGCTTTCACAAAGCCACTGATGCGTAC	481
QY	56	lleproalaarpleuProleuCyuhisthvalglytyllyrargmetargleuproasn	75
Db	482	ATCCCGCGGACCTGCGGCTGGCCACAACGCGGGCTCAAGAAAGATGCTGCGCCAAAC	541
QY	76	leuileugluhieglnserleualaagluvalylsglnglnalasersttrpleuProleu	95
Db	542	CTGCTGAGAGCAGAACCATGGCGGAGTGAAGACGAGCGCGACGCTGGGCTGCTCG	601
QY	96	leuualylrargCyuhisSerzasprrhnglnalPheleuCyserleuPhealaproval	115
Db	602	CTCAACAAAGAACTGGCACGCGCGACCCCAAGGCTTCTCTGTGCTGCTGCCCCCGTC	661
QY	116	CysleuaparargProiletryrProCyargserleuCyrgluualavalargalaglyCys	135
Db	662	TGCCCTGGACCGGCCCATCTACCCCGTGTGGCTGCGTGGAGCGCGTGGCGGACTCGC	721
QY	136	AlaPrleuemetglualatrglyrPheProTrrProglumetleuhisCyuhislyrPhe	155
Db	722	GAGCGGCTCATGCACTTCTGCGGCTTCTCACTGCGCCCGAAGAGCTTAAGTGACAAAGTTC	781
QY	156	ProleuapararpleuCyvilelalavalalgnPhegluhis---leuProalaarhrla	174
Db	782	CCC---GAGGGGAGCTGTGCATTCGCATAGACCGCGCCCATCCACCGAAAGCTTCGAA	838
QY	175	ProProvalThrlyleleCyualaglnCyrglmetgluhiseralasapolyuemet	194
Db	839	CCCCAAGGACACACGCTGTGTCTCCCTCTGACAAACAGTGAATCTGAGGCCACTATT	898
QY	195	gluglnmetCysSerSerzasprrheValvallyrMetarglilelyeglnileylleu	214
Db	899	GAACTCTCTGCGCAGCGAGTTTGCATGAGAGTGAATAATGAAGAGTGAATAAAGAA	958
QY	215	AenlglaarpararglyleuilelglyalaglnlyrlyrlyrlyrleuileuLyrrProgl	234
Db	959	AATGGCGCAACAAATAATTTGTC---CCCAAGAAAGAAAGGCCCTTAAGTTGGGGGCC	1012

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Oy 235 LeuIyVaRgYySaPRTxLySaRgLeuValIeUHiMeClySaBnJyAlaGlyCySPro 254
Db 1013 ATCAAGAAGAGACCTCGAAGAACCTTGTCTTACTCTGAAGATGGGCTACTCTCC 1072
Oy 255 CySProGlnLeuApsSerLeuAlaGlySerPheLeuValMeGlyAlaRgYyValaBpGly 274
Db 1073 TGCCACAGCTGGAGCAACCTCAGCCACCACTTCTCATCATGAGCGCGCAAGGTGAAGAGC 1132
Oy 275 GlnLeuLeuMeAlaValIyTRaGTYpPaapLyLySaBnJyAlaGlnMeClySPheaAla 294
Db 1133 CAGTACTGTGACGGCGCATCCCAAGTGGAGCAAGAAAAACAAGAGATTCAAAAACTTC 1192
Oy 295 ValIySPheMeTPheSerTYrProCySPeSerLeuTYrPProPhe 310
Db 1193 ATGAAGAAATGAATAAACCATGAGTCCCACTTTCAGTCCGTGTTT 1240

RESULT 9
US-10-301-764-18
: Sequence 18, Application US/10301764
: Publication No. US20040039184A1
: GENERAL INFORMATION:
: APPLICANT: Umanaky, Samuil
: Melkonyan, Hovsep
: TITLE OF INVENTION: A FAMILY OF GENES ENCODING
: APOPOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
: METHODS OF USE THEREOF
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/301,764
: FILING DATE: 20-No. US20040039184A1-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/937,067
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Lehnhardt, Susan K.
: REGISTRATION NUMBER: 33,943
: REFERENCE/DOCKET NUMBER: 23647-20018.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 813-5600
: TELEFAX: (650) 494-0792
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1308 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-301-764-18

Alignment Scores:
Pred. No.: 1,44e-104 Length: 1308
Score: 924.50 Matches: 179
Percent Similarity: 72.8% Conservative: 51
Best Local Similarity: 56.6% Mismatches: 77
Query Match: 53.4% Indels: 9
DB: Gaps: 6

US-10-768-566-1 (1-317) x US-10-301-764-18 (1-1308)

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Job time : 915 secs

Percent Similarity: 74.1% Conservative: 50
 Best Local Similarity: 57.9% Mismatches: 70
 Query Match: 53.0% Indels: 10
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US-10-768-566-1 (1-317) x US-10-466-136-2 (1-942)

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DB      22 GGGGGCGCGCGCGCGCGCGCGCTGGGGCGTGGCTGCTG--GCCTGGCGCGCGCTTCTGGC 78
QY      28 ARG-----CYAGLUGLUTYRAPTYYTYRGLYTRPGINALAGLU-----PROLEUHS 43
DB      79 CGTGGGCTGGCAGCAGATACGACTGAGCTTCAGTCGAGATCGGCCGTACCGCCGTACCGAG 138
QY      44 ---GLYARGSERLYSERLYSPROFGLNCYLEUASPILEPROLAAAPLEUPROLEU 62
DB      139 AGCGGGCGCTTCTTACACCAAGCCACTTCAGTGGTGAACATCCCGCGGACCTGCGGCTG 198
QY      63 CYSHISTHRVALGLYTRYLYSARGMEARGLEUPROASNLEUAGLUHISGLUSERLEU 82
DB      199 TGCACAACGTGGGCTACCAAGATGTGTGCTGCCAAGCTGCTGGAGCAGACCATG 258
QY      83 ALAAGLVALLYSGINGINALASERSETTRPLEUPROLEUENALALYSARGCYSHISER 102
DB      259 GCGAGGTGAGAGCAGGCGCAGCAGCTGAGTGCCTGCTCAACAAAGAACTGCCAGGCC 318
QY      103 AAPTHG1VALPHELEUCYSESLLEUPHEALAPROVALCYSEUASPARPROILETYR 122
DB      319 GGGACCCAGAGTCTTCTCTGCTGCTCTTCCGCCCTGCTGCTGAGCCGCCCATCTAC 378
QY      123 PROCYARGSERLEUCYSGIUALAVALARGALAGLYCYALAPROLEUWETGLUALATYR 142
DB      379 CCGTGTGGTGGCTGCGAGCGCGGTGGGAGCTGTGGAGCGGCTCATGCACTTCTTC 438
QY      143 GLYPHEPROTRPFGIULWETLEUHSICYSHISLYSPHEPROLEUASPARLEUCYS 162
DB      439 GGCCTTCTACTGGCCCGAGATGCTTAAGTGTGACAAAGTCCCG--GAGGGGGAGCTCTGC 495
QY      163 ILEALAVALAGLPHNEGLYHS---LEUPROALATHRALAPROVALTHRLYSILECYV 181
DB      496 ATGCGCATGACGCCGCCCAATGCCACCGAAGCCTCCAGGCCCCCAAGCACAACGCTGTGT 555
QY      182 ALAGLNCYSGIULWETGLUHSERIALAAPGLYLEUWETGLUWETCYSESERSEARP 201
DB      556 CCTCCCTGTGACAAACAGATTGAATCTGAGGCCCATGTAACATCTGTGTGCCAGCGAG 615
QY      202 PHEVALVALYWEKARGILEYSGIULILEYSEILEGLUANGLYASPARGLYSEULIE 221
DB      616 TTTCACACTGAGATGAAATAAAGAAAGTGAATAAAGAAATAATGCGACAAAGAAATTGTC 675
QY      222 GLYALGILLYSELYSELYSELYSELYSELYSPROGLYPROLEUYSARGLYSAPTHRLYS 241
DB      676 -----CCCAAGAAAGAAAGCCCTGAGAGTGGGGCCCATCAAGAAAGAGACTGAGAG 729
QY      242 ARGLEUVALLEUHSIMETLYSAENGLYALAGLYCYAPROCYSPROGLINLEUASERLEU 261
DB      730 AAGCTTGTGTGTAAGTGAAGATGGGGCTGACTGTCCCTGCCACCAAGCTGGAGCAACTC 789
QY      262 ALAAGLYSERPHELEUVALMETGLYARGLYVALASPGLYGLINLEULEUWETALAVAL 281
DB      790 AGCCACCACTTCTCATCATGAGGCGCCCAAGGTGAAGAGCCAGATCTTGCTGACGGCCATC 849
QY      282 TYRARGTRAPASLYSELYSALNLYSGIULWETLYSPHEALVALALYSPHEWETPHESEITYR 301
DB      850 CACAAGTGGAGCAAGAAAGAAAGAGTTCAAAAACCTTCATGAAGAAATGAAAAACCAT 909
QY      302 PROCYSERLEUTYRTRYRPROPHEPHE 310
DB      910 GAGTGCCCAACCTTTCAGTCCGTGTTT 936

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Search completed: March 23, 2006, 07:20:54

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 07:05:10 ; Search time 390 Seconds
(without alignments)
1895.258 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730

Sequence: 1 MRNAAGGVRTPALALLG.....MFSYPCSLYPPFYGAEPH 317

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 10.0, Fgapext 0.5
Delop 6.0, Delext 7.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications_NA_New -OPMT=faetap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -HOST=abse04
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-NO_WAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications_NA_New.*

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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						
1	916	52.9	4469	9	US-11-245-147-203	Sequence 203, App
2	916	52.9	4608	8	US-10-821-234-137	Sequence 137, App
3	624	36.1	1382	9	US-11-245-147-197	Sequence 197, App
4	621.5	35.9	2379	6	US-09-925-065A-678403	Sequence 678403,

5	615.5	35.6	926	9	US-11-245-147-5	Sequence 5, Appli
6	457	26.4	882	9	US-11-245-147-80	Sequence 80, Appli
7	453	26.2	475	12	US-11-004-762-19	Sequence 19, Appli
8	434	25.1	631	6	US-09-925-065A-68204	Sequence 68204, A
9	420.5	24.3	1745	6	US-11-051-770-28	Sequence 28, Appli
10	285	16.5	1291	12	US-11-184-005-23	Sequence 23, Appli
11	283.5	16.4	2374	12	US-11-184-005-1	Sequence 1, Appli
12	280	16.2	2184	12	US-11-054-281-35	Sequence 35, Appli
13	279.5	16.2	1484	12	US-11-184-005-3	Sequence 3, Appli
14	276	16.0	2561	12	US-11-127-877-26	Sequence 26, Appli
15	269	15.5	2811	12	US-11-067-531-154	Sequence 154, App
16	269	15.5	2814	12	US-11-054-281-21	Sequence 21, Appli
17	268.5	15.5	1935	12	US-11-136-527-186	Sequence 186, App
18	267	15.4	1983	9	US-11-245-147-206	Sequence 206, Appli
19	263.5	15.2	1944	9	US-11-245-147-49	Sequence 49, Appli
20	263	15.2	4350	9	US-11-245-147-124	Sequence 124, App
21	263	15.2	4350	9	US-11-245-147-125	Sequence 125, App
22	263	15.2	4350	9	US-11-245-147-205	Sequence 205, App
23	253.5	14.7	7391	12	US-11-152-366-17	Sequence 17, Appli
24	253.5	14.7	7391	12	US-11-169-041-5	Sequence 5, Appli
25	253.5	14.7	7392	9	US-11-245-147-177	Sequence 177, App
26	253.5	14.7	7392	9	US-11-245-147-208	Sequence 208, App
27	250	14.5	4770	12	US-11-136-527-299	Sequence 299, App
28	247	14.3	1898	12	US-11-136-527-2690	Sequence 2690, Ap
29	226.5	13.1	1076	12	US-11-128-061-1138	Sequence 1138, Ap
30	226.5	13.1	1076	12	US-11-128-049-1138	Sequence 1138, Ap
31	210.5	12.2	2607	12	US-11-136-527-630	Sequence 630, App
32	207	12.0	2820	9	US-11-245-147-204	Sequence 204, App
33	207	12.0	2820	12	US-11-186-284-188	Sequence 188, App
34	207	12.0	2840	12	US-11-054-281-23	Sequence 23, Appli
35	206	11.9	3375	9	US-11-245-147-178	Sequence 178, App
36	206	11.9	3375	9	US-11-245-147-207	Sequence 207, App
37	161	9.3	4804	12	US-11-067-811-3	Sequence 3, Appli
38	156	9.0	6004	12	US-11-136-527-5450	Sequence 5450, Ap
39	156	9.0	604	12	US-10-750-185-38928	Sequence 38928, Ap
40	150	8.7	1166	8	US-10-750-185-38928	Sequence 38928, A
41	150	8.7	1166	8	US-10-750-623-58928	Sequence 58928, A
42	149.5	8.6	1853	8	US-10-750-185-51334	Sequence 51334, A
43	149.5	8.6	1853	8	US-10-750-623-51334	Sequence 51334, A
44	130	7.5	1302	12	US-11-152-366-18	Sequence 18, Appli
45	119.5	6.9	1815	8	US-10-750-185-48508	Sequence 48508, A

ALIGNMENTS

RESULT 1
US-11-245-147-203
; Sequence 203, Application US/11245147
; Publication No. US20060030541A1
GENERAL INFORMATION:
APPLICANT: GARCIA, TERESA
APPLICANT: ROMAN ROMAN, SERGIO
APPLICANT: BARON, ROLAND
APPLICANT: CALI, KATHERINE
APPLICANT: THEILHABER, JOACHIM
APPLICANT: CONNOLLY, TIMOTHY
APPLICANT: JACKSON, AMANDA
APPLICANT: BUSHNELL, STEVEN
APPLICANT: RAWADI, GEORGES
TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
FILE REFERENCE: 37991-0023
CURRENT APPLICATION NUMBER: US/11/245,147
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,400
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 203
LENGTH: 4469
TYPE: DNA
ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: Homo sapiens secreted frizzled-related protein 1
; OTHER INFORMATION: (SFRP1), mRNA.
US-11-245-147-203

Alignment Scores:
Pred. No.: 8,37e-75 Length: 4469
Score: 916.00 Matches: 179
Percent Similarity: 72.0% Conservative: 50
Best Local Similarity: 56.3% Mismatches: 77
Query Match: 52.9% Indels: 12
DB: 9 Gaps: 7

US-10-768-566-1 (1-317) x US-11-245-147-203 (1-4469)
QY 2 ArgAlaAlaAlaAlaAlaGly-----GlyValArgThrAlaAlaLeuAlaLeu 18
DB 24 AGAGCCGCGATGGGCGATCGGCGCGCAGCGAGGGGGCGCGCGGGCGCTGGGGCTGCTG 353
QY 19 -----LeuGlyAlaLeuAlaIstPrAlaPrAlaArgCyseGluGluIuYrAspTYrTYrGly 36
DB 354 CTGGGCGTGGGCGCGCGCTTCTGGCCGTGGGCTGGCGCAGGAGTACGACTACGTAGAC 413
QY 37 TrpGlnAlaGlu-----ProLeuHis---GlyArgSerTYrSerLYsPProGlnCyse 53
DB 414 TTCAGTGGACATCGGCGCGCTTACCAAGACGCGCGCTTCTTACACCAAGCCACTCAGTGC 473
QY 54 LeuAspIleProAlaAspLeuProLeuCyseHisIsthrValGlyTYrLYsArgMetArgLeu 73
DB 474 GTGGACATCCCGCGGACCTGGCGGCTGTGCCAAGTGGGCTTACAGAAATGGTCTG 533
QY 74 ProAsnLeuLeuGluHisGluSerLeuAlaGluValLYsGlnGlnAlaSerSerTrpLeu 93
DB 534 CCCAAGCTGCTGAGACAGACGACATGCGGAGGTGAAGACACAGGCCAGCGTGGG 593
QY 94 ProLeuLeuAlaLYsArgCyseHisSerAspThrGlnValPheLeuCYseSerLeuPheAla 113
DB 594 CCCGCTCCACAGAACTGCCACGCGCGGACCCAGCTTCTGCTGCTGCTGCTGCGG 653
QY 114 ProValCYsLeuAspArgProIleTYrProCYsArgSerLeuCYsGluAlaValAlaArgAla 133
DB 654 CCCGCTGCTGCGACCGCGCCCATCTACCGCTGTGCTGCTGCTGCGAGCCGTGGCGAC 713
QY 134 GlyCYsAlaProLeuMetGluAlaTYrGlyPheProTrpProGluMetLeuHisCYsHis 153
DB 714 TCGTCGAGCCGGTATGAGTCTTCGGCTTCTACTGGCCCGAGATGTTAAAGTGTAC 773
QY 154 LYsPheProLeuAspAsnAspLeuCYsValIleAlaValGlnPheGlyHis---LeuProAla 172
DB 774 AAGTCCCG---GAGGGGACGCTGCATCGCCATGACCGCCGCCCAATGCCACCGAAAGCC 830
QY 173 ThrAlaProProValThrLYsIleCYsValAGlnCYsGluMetGlnHisSerAlaAspGly 192
DB 831 TCCAAAGCCCAAGGACACAGGATGTGTCTCCCTGTGACAGAGTGAATCTGAGGCC 890
QY 193 LeuMetGluGlnMetCYsSerSerAspPheValValLYsMetArgIleLYsGlnLYs 212
DB 891 ATCATGAACATCTGTGTCGACGAGTGTGCACTGAGAGTGAATAAATAAAGAGTAAA 950
QY 213 IlegLYsAsnGlyAspArgLYsLeuIlegLYsAlaGlnLYsValLYsValLYsLeuLYsPro 232
DB 951 AAAGAAATGGCGAAGAAAGATTGTC-----CCCAAGAAAGAAAGCCCTGGAAGTTGG 1004
QY 233 GlyProLeuLYsArgLYsAspThrLYsArgLeuValLYsMetLYsValAsnGlyAlaGly 252
DB 1005 GGGCCATCAAGAAAGAGACCTGAAGAGCTTGTGCTTACCTAGAGATGGGGCTGAC 1064
QY 253 CyseProCYsProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArgLYsVal 272
DB 1065 TGTCTCTGCGACACAGGTGGAACAACCTCAGACCACTTCTCATATGAGCGCGCAAGGTG 1124
QY 273 ArgGlyGlnLeuLeuLeuMetAlaValTYrArgTrpAspLYsValAsnLYsGluMetLYs 292
```

```
DB 1125 AAGAGCCGACTCTGTCACGCGCATCCACAAAGTGGCAAGAAACAAAGAGTTCAA 1184
QY 293 PheAlaValLYsPheMetPheSerTYrProCYsSerLeuTYrTYrPhePhe 310
DB 1185 AACTTCATGAAGAAATGAAAACCATGATGAGGCCCACTTTCAGTCCGTGTT 1238

RESULT 2
US-10-821-234-137/c
; Sequence 137, Application US/10821234
; Publication No. US2005025114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pf_seq_genes Version 1.0
; SEQ ID NO 137
; LENGTH: 4608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-137

Alignment Scores:
Pred. No.: 8,68e-75 Length: 4608
Score: 916.00 Matches: 179
Percent Similarity: 72.0% Conservative: 50
Best Local Similarity: 56.3% Mismatches: 77
Query Match: 52.9% Indels: 12
DB: 8 Gaps: 7

US-10-768-566-1 (1-317) x US-10-821-234-137 (1-4608)
QY 2 ArgAlaAlaAlaAlaAlaGly-----GlyValArgThrAlaAlaLeuAlaLeu 18
DB 4315 AGAGCCGCGATGGGCGATCGGCGCGCAGCGAGGGGGCGCGCGGGCGCTGGGGCTGCTG 4256
QY 19 -----LeuGlyAlaLeuAlaIstPrAlaPrAlaArgCyseGluGluIuYrAspTYrTYrGly 36
DB 4255 CTGGGCGTGGGCGCGCGCTTCTGGCCGTGGGCTGGCGCAGGAGTACGACTACGTAGAC 4196
QY 37 TrpGlnAlaGlu-----ProLeuHis---GlyArgSerTYrSerLYsPProGlnCyse 53
DB 4195 TTCAGTGGACATCGGCGCGCTTACCAAGACGCGCGCTTCTTACACCAAGCCACTCAGTGC 4136
QY 54 LeuAspIleProAlaAspLeuProLeuCyseHisIsthrValGlyTYrLYsArgMetArgLeu 73
DB 4135 GTGGACATCCCGCGGACCTGGCGGCTGTGCCAAGTGGGCTTACAGAAATGGTCTG 4076
QY 74 ProAsnLeuLeuGluHisGluSerLeuAlaGluValLYsGlnGlnAlaSerSerTrpLeu 93
DB 4075 CCCAAGCTGCTGAGACAGACATGCGGAGGTGAAGACAGCGCCAGCGAGCTGGG 4016
QY 94 ProLeuLeuAlaLYsArgCyseHisSerAspThrGlnValPheLeuCYseSerLeuPheAla 113
DB 4015 CCCCGCTCCACAGAACTGCCACGCGCGGACCCAGCTTCTGCTGCTGCTGCTGCGG 3956
QY 114 ProValCYsLeuAspArgProIleTYrProCYsArgSerLeuCYsGluAlaValAlaArgAla 133
DB 3955 CCCGCTCTCTGAGACCGCGCCATCTACCGCTGTGCTGCTGCTGCGAGCGCTGGCGAC 3896
QY 134 GlyCYsAlaProLeuMetGluAlaTYrGlyPheProTrpProGluMetLeuHisCYsHis 153
DB 3895 TCGTCGAGCCGGTATGAGTCTTCGGCTTCTACTGGCCCGAGATCTTAAAGTGTAC 3836
QY 154 LYsPheProLeuAspAsnAspLeuCYsValIleAlaValGlnPheGlyHis---LeuProAla 172
```

Db	3835	AAAGTTCCCG---	GAGGGGGAGAGTGTGCATGCGCATGAGCGCGCCAAATGCGCACCGGAAGCC	37719
Qy	173	ThrlaPpProProValThrlYsIleCysAlaIcngYsgIumetGluHiseSerAlaaspGly	192	
Db	3778	TCCAAGACCCCAAGGACCAACGGGTGTCTCCTCCGTGTGACCAACGAGTTGAATTCGAGGCC	3719	
Qy	193	LeuMetGluGlnMetCysSerSerAspPheValValLyMetValGlyGluIleYs	212	
Db	3718	ATCATGTGAACATCTCTGTGCAGCGAGATTTCACATGAGAGATGAATAATAAAGAGTGA	3659	
Qy	213	IlleGluasnGlyAspArgLyLeuIleGlyValGlnLybLybLyLeuLeuLeuPro	232	
Db	3658	AAAAAAATGCGCGACAGAGAAATGTC-----CCCAAGAAAGAGAACCCCTGAAGTTG	3605	
Qy	233	GlyProLeuLeuYsArgLyAspThrLyArgGluValLeuHismetLyAsnGlyAlaGly	252	
Db	3604	GGGCGCCATCAAGAAAGAGAGACCTTGAAAGCTTGCTGCTGACCTGAAACAAATGGGGCTGAC	3545	
Qy	253	CysPProCysProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArgLybVal	272	
Db	3544	TGTCCCTGTGCCACAGCTGTGACCACTTGACCACTTCCTCATCATGAGGCGCGCAAGGTG	3485	
Qy	273	AspGlyGlnLeuLeuLeuMetAlaValYlyArgTrpAspLybLyAsnLyGlnmetYs	292	
Db	3484	AAGAGCCAGTACTTGCTACGGCCATCCACAAAGTGGACAGAAACAAAGAGATTCAA	3423	
Qy	293	PheAlaValLyPheMetPheSerTyTrProCysSerLeuTyTrYTrProPhePhe	310	
Db	3424	AACCTTCATGAAGAAATATAAAAACCATAGTGTGCCCACTTTCAGTCCGTGTTT	3371	

```

RESULT 3
US-11-245-147-197
: Sequence 197, Application US/11245147
: Publication No. US20060030541A1
GENERAL INFORMATION:
: APPLICANT: GARCIA, TERESA
: APPLICANT: ROMAN ROMAN, SERGIO
: APPLICANT: BARON, ROLAND
: APPLICANT: CALL, KATHERINE
: APPLICANT: THEILHAUER, JOACHIM
: APPLICANT: CONNOLLY, TIMOTHY
: APPLICANT: JACKSON, AMANDA
: APPLICANT: BUSHNELL, STEVEN
: APPLICANT: RAMADI, GEORGES
: TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
: FILE REFERENCE: 37991-0023
: CURRENT APPLICATION NUMBER: US/11/245,147
: CURRENT FILING DATE: 2005-10-07
: PRIOR APPLICATION NUMBER: PCT/IB02/02211
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: 60/281,400
: PRIOR FILING DATE: 2001-04-05
: NUMBER OF SEQ ID NOS: 246
: SOFTWARE: PatentIn Ver. 3.2
: SEQ ID NO 197
LENGTH: 1382
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Homo sapiens secreted frizzled-related protein 2
US-11-245-147-197

Alignment Scores:
Pred. No.: 3,34e-48 Length: 1382
Score: 624.00 Matches: 132
Percent Similarity: 57.0% Conservative: 51
Best local Similarity: 41.1% Mismatches: 97
Query Match: 36.1% Indels: 41
DB: 9 Gaps: 7
US-10-768-566-1 (1-317) x US-11-245-147-197 (1-1382)

```

[illegible]

Oy 292 S 292
Db 1073 G 1073

RESULT 4
US-09-925-065A-678403
; Sequence 678403, Application US/09925065A;
; Publication No. US20040181048A1
; GENERAL INFORMATION:

RESULT 4
US-09-925-065A-678403
; Sequence 678403, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 678403
LENGTH: 2379
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-678403
```

```
Alignment Scores:
Pred. No.: 1,08e-47 Length: 2379
Score: 621.50 Matches: 133
Percent Similarity: 57.0% Conservative: 17
Best Local Similarity: 51.3% Mismatches: 75
Query Match: 35.9% Indels: 54
DB: Gaps: 7
```

US-10-768-566-1 (1-317) x US-09-925-065A-678403 (1-2379)

```
QY 37 TTPGlnAlaGluProLeuHnIsgLyRgsSerTyRserTyProGlnCyLeuAap-11 56
DB 233 TGGGAATCATCTCCCA---GAGATCAGAGATCCAGCTTCTCCATCAGAGATCCCT 309
QY 56 eProAlaAapLeuProLeuCyHnIsgThyValGlyTyRlyAaRgMeArGleuProAaHle 76
DB 310 TCCAGAGCATGGCGGCCAGATGCCATCCACTCCT-TATCCCTCCCTGGGAGCCCCACAT 368
QY 76 uLeuGlnHnIsgLysSerLeuAlaGluVallysgLnglnAlaSerSerTyRleuProleu 96
DB 369 GCTGTCTCATCAAGAGCTC-----TCCACCCCTGCTTTGGT 404
QY 96 uAlaIyAaRgCyHnIsgSerArThrGlnValPheLeuCySerLeuAapPheAlaProValCy 116
DB 405 G-----TCTCAAGAGGCTTGAATGAAATGATGCAATTCACGAGCTCAG 443
QY 116 eLeuAaPArGProIleTyRPro-----CyAaR 125
DB 444 AAGCTCTCAATCCCTCAATTTCCCTCTGTACTGAGATGAAACGTAGTGTCTCC 503
QY 125 gSerLeuCyGlnAlaValAaRgAlaGly-----CyAaIaProLeuMeGlnAl 141
DB 504 TTGAGAGTGCAGCATGATTAAGTCTCATTAATGAAATGTGCC-----CTAGAGGC 557
QY 141 aTyRgLyPheRProTyRProGlnMeLeuHnIsgCyHnIsgTyRPhRProLeuAaPArAaPle 161
DB 558 TCCACCCCTTCCAGAGCCCGCAGGAGCATC----- 585
QY 161 uCyAileAlaValGlnPheGlnIyAeUProAlaThRAlaProProValThRlyAileCy 181
DB 586 -----AGGCTCCCGAGCCCGAAGGTCCAGAAACACACACACACATC 623
QY 181 eAlaGlnCyGlnMeGlnHnIsgSerAlaAaRgLyLeuMeGlnGlnMeCySerSerAa 201
DB 624 TGTGCCACCAAGCATCCACAGATCTGACCATTTCCCAATTTGCCCTGTCTTCTTC 683
QY 201 pPhe-ValIyAaRgMeArGlyIyGlnIyAlaIyGlnGlnGlnIyAaPArGlyLeuI 221
DB 684 CCACAGTGTCAAAATGCCATCAAGAGATCAAGTAAAGATGGGGAGCCGAAAGCTGA 743
```

```
QY 221 IeGlyAlaGlnIyAaRgMeArGlyIyGlnIyAlaIyGlnGlnIyAaPArGlyLeuI 241
DB 744 TTGGAGCCCAAGAAAGAAAGAGAGGCTCAAGCCGGGCGCCCTGAAAGCGACACCA 803
QY 241 yAaRgLeuValLeuHnIsgMeTyRysAaGlnIyAaGlyCyRProCyProGlnIyAaPAr 261
DB 804 AGGCGCTGTGTGACATGAAGAATGGCGGGGTGCTCCCTGCGCCACAGCTGAGCAGCC 863
QY 261 eAlaGlySerPheLeuValMeGlyAaRgLyValAaPglYglnIyAaPArAaPle 281
DB 864 TGGCGGGAGAGCTTCTGTGATCGGCGCGCAAGTGAAGAGAGAGTGTGATGAGTGTCT 923
QY 281 aTyRArGTTPAaPlyAaRgLyAaRgLyMeTyRPhRAlaValIyAaPArPheMeTyR 301
DB 924 TCTACCGCTGGGACAAAGAAATGAAGATGAAGATTTGACATCAATTCATGTTCTCT 983
QY 301 yRProCySerLeuTyRProPheTyRgLyAlaAlaGlnIyAaPAr 317
DB 984 ACCCTGCTCCCTCTACTACCTTTCTTCTACGGGGCGGCGAGAGCCCAAC 1033
```

RESULT 5
US-11-245-147-5
Sequence 5, Application US/11245147
Publication No. US20060030541A1

GENERAL INFORMATION:
APPLICANT: GARCIA, TERESA
APPLICANT: ROMAN ROMAN, SERGIO
APPLICANT: BARON, ROLAND
APPLICANT: CALL, KATHERINE
APPLICANT: THEILHABER, JOACHIM
APPLICANT: CONNOLLY, TIMOTHY
APPLICANT: JACKSON, AMANDA
APPLICANT: BUSHNELL, STEVEN
APPLICANT: RAMADI, GEORGES
TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
FILE REFERENCE: 37991-0023
CURRENT APPLICATION NUMBER: US/11/245,147
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,400
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO: 5
LENGTH: 926
TYPE: DNA
ORGANISM: Mus musculus
US-11-245-147-5

Alignment Scores:
Pred. No.: 1,29e-47 Length: 926
Score: 615.50 Matches: 126
Percent Similarity: 61.8% Conservative: 52
Best Local Similarity: 43.8% Mismatches: 93
Query Match: 35.6% Indels: 17
DB: Gaps: 7

US-10-768-566-1 (1-317) x US-11-245-147-5 (1-926)

```
QY 13 AAlaAlaLeuAlaLeuLeuGlyAlaLeuHnIsgThRAlaProAlaAaRgCyGlnGlyTyR 32
DB 36 GCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 95
QY 33 AaRgTyRgLyTyRProGlnAlaGluProLeuHnIsgLyRgsSerTyRserTyRProGln 52
DB 96 TTCTCTTGTGCTC---CAGCCCGAGCTTCTCTCAACAGCGCAACCTGCAAGCTCC----- 146
QY 53 CyLeuAaPArIleProAlaAaPLeuProLeuCyHnIsgThRValGlyTyRlyAaRgMeArG 72
DB 147 -----ATCCCGGCAACCTGCAAGCTGTGCGCAGCGCAATGACATGACCAAGCTGCG 197
```



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QY 73 LeuProAvalLeuGluHISgluSerLeuAlaGluValylsGlnGlnAlaSerSerTrp 92
Db 198 CTGGCCAACTGCTGGGCGACAGACCATGAAGAGAGTCTGGAGCAGGCGGCGCTGG 257
QY 93 LeuProLeuLeuAlaValArgCysHisSerAspThrGlnValPheLeuCysSerLeuPhe 112
Db 258 ATTCCGCTGCTCATGAAGAGTGCACCCGCGACACCAAGATCTCTGCTCGCTCTTC 317
QY 113 AlaProValCys-----LeuAspArgProIleTyProCysArgSerLeuCysGlu 129
Db 318 GCCCTGCTGCTGCTGCGACGACCTAGATGAAGACCATCAGCCGCTGCTGCTGCGTG 377
QY 130 AlaValArgAlaGlyCysAlaProLeuMetGluAlaTyArgIlePheProTrpProGluMet 149
Db 378 CAGGTAAAGACCGCGCGCGCGCTCATGTCCGCTTCCGCTTCCGCGCGACAGCAG 437
QY 150 LeuHisCysHisIlePhePheProLeuAspAsnAspLeuCysIleAlaValGlnPheGlyHis 169
Db 438 CTGAGAGTGCAGCGCTTCCGCGACGACCAACGACCTCGCATCCCTCCCTAGTACGAC 497
QY 170 -----LeuProAlaThr-----AlaProProValThrIleGlyValAlaGlnCysGlu 185
Db 498 CACCTCTGCTGGCGCGACAGAGAGGCTCC-----AAGGTGTGAAGCTGCAAA 548
QY 186 MetGluHisSerAlaAspGly--LeuMetGluGlnMetCysSerSerAspPheValVal 204
Db 549 ACCAGAAATGAGGACGACCAACGACATCATGAAACCTTTGTAATAATGACTTCGACAG 608
QY 205 IysMetArgIleIleArgIleIleValIleGluAsnGlyAspArgIleLeuIleGlyAlaGln 224
Db 609 AAATCAAGTAGTAAGAGATTAACGTACATCAACAGACAGACCAAGATCATCTCGAGACA 668
QY 225 IysIleValIleValLeuLeuIleIlePheProGlyProLeuIleValArgPheThrIleVal 244
Db 669 AAGAGCAACCACTTACCAAGCTGAACGGGCTGTCCGAAAGGACCTGAAGAAATCCGCG 728
QY 245 LeuHisMetIleValAsnGlyIleAlaGlyCysProCysProGlnIleAspSerLeuAlaGlySer 264
Db 729 CTGTGGCTCAAGACAGCGCTGCACTGTGAGAGATGAACACATCAACGCTCCG 788
QY 265 PheLeuValMetGlyArgIleValIleAspGlyGlnLeuLeuMetAlaValTyArgTrp 284
Db 789 TATCTGTCATGTGAGCAAGAGCAGGCGGCGAGCTGTGTATCACTCCGTAAGAAACGCTGG 848
QY 285 AspIleValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 292
Db 849 CAGAAAGGCGCAGAGAGATTCAAG 872

RESULT 6
US-11-245-147-80
; Sequence 80, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHAUER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAMADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 60

```

```

; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (615)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-11-245-147-80

Alignment Scores:
Pred. No.: 7,08e-33 Length: 882
Score: 457.00 Matches: 105
Percent Similarity: 59.64 Conservative: 28
Best Local Similarity: 47.14 Mismatches: 67
Query Match: 26.44 Indels: 23
DB: 9 Gaps: 8

US-10-768-566-1 (1-317) x US-11-245-147-80 (1-882)
QY 2 ArgAlaAlaAlaAlaAlaGlyGlyValArgThrAlaAlaLeuAlaLeuLeuGluValAla 21
Db 255 CGCGCCAGATGCTGCGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 314
QY 22 LeuHisTrpAlaProAlaArgCysGluGluIleValArgIleTyArgIleTyArgIleAlaPro 41
Db 315 CTGCTGGGCTGGGCGCGGCGGCTCTCTCTT-----TGCCAGCCGCACTT 362
QY 42 Leu-HisGlyArgSerTySerIlePheProGlnCysLeuAspIleProAlaAspLeuPro 61
Db 363 CTCCTACAGCCGACCAATTCGACGCC-----ATCCGCGCAACCTGCA 407
QY 61 OleuCysHisThrValGlyTyIleValArgMetArgLeuProAsnLeuLeuGluHisGlyIle 81
Db 408 GCTGTGCGACGCGCATCGAATACAGACATGCGGCTGCCAAGCTGCTGGCCAGAGAC 467
QY 81 rIleuAlaGluValIleGlnGlnAlaSerSerTrpLeuProLeuLeuAlaValArgCysHis 101
Db 468 CATGAAGAGGTGTGAGAGAGCGCGGCGCTTGATCCGCGTGTGATGAAGACATGCGCA 527
QY 101 sSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCys-----LeuAs 118
Db 528 CCCGACACCAAGAAAGTTCCTGTGCTGCTCTTCCGCCCCCGCTGCTGCTGATGACTTGA 587
QY 118 PArgProIleTyProCysArgSerLeuCysGluAlaValArgAlaGlyCysAlaProLe 138
Db 588 CAGACACATCCAGCCATGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 647
QY 138 uMetGluAlaTyArgIlePheProTrpProGluMetLeuHisCysHisIleValPheProLeuAs 158
Db 648 CATGTCCGCG-----TTCCCTGCGCGGACATGCTTGAAGTCCGACCGTTTCCCGAGGA 701
QY 158 PAsnAspLeuCysIleAlaValGlnPheGlyHis-----LeuProAlaThr-----Al 174
Db 702 CAACGACCTTTCATCCCTCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 761
QY 174 AProProValThrIleValIleCysAlaGlnCysGluMetGluHisSerAlaAspGly---Le 193
Db 762 TCCA-----AAGTATGTGAAGCCCTGCAAAATTAATTAATGAATGAACAGACAT 812
QY 193 uMetGluGlnMetCysSerSerAspPheValValIleValMetArgIleIleValIleValIle 213
Db 813 AATGAAAGCTTTGTAAATAATGATTTCGACTGAAATTAATAAGTAAGTAATTAACCTA 872
QY 213 eGluAsn 215
Db 873 CATCAAC 879

RESULT 7
US-11-004-762-19
; Sequence 19, Application US/11004762
; Publication No. US2006003053A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett

```

```
/ APPLICANT: Madeline M. Butler
/ APPLICANT: Nicholas M. Dean
/ APPLICANT: Kenneth W. Dobie
/ APPLICANT: Joshua Finger
/ APPLICANT: Ravi Jain
/ APPLICANT: Robert McKay
/ APPLICANT: Brett P. Moria
/ APPLICANT: Kathleen Myers
/ TITLE OF INVENTION: Compositions and their uses directed to bone growth modulators
/ FILE REFERENCE: BIO00050US
/ CURRENT APPLICATION NUMBER: US/11/004,762
/ CURRENT FILING DATE: 2004-12-03
/ PRIOR APPLICATION NUMBER: US 60/527,370
/ PRIOR FILING DATE: 2003-12-04
/ PRIOR APPLICATION NUMBER: US 60/527,173
/ PRIOR FILING DATE: 2003-12-04
/ PRIOR APPLICATION NUMBER: US 60/527,172
/ PRIOR FILING DATE: 2003-12-04
/ PRIOR APPLICATION NUMBER: US 60/527,420
/ PRIOR FILING DATE: 2003-12-04
/ PRIOR APPLICATION NUMBER: US 60/527,174
/ PRIOR FILING DATE: 2003-12-04
/ PRIOR APPLICATION NUMBER: US 60/527,397
/ PRIOR FILING DATE: 2003-12-04
/ NUMBER OF SEQ ID NOS: 680
/ SOFTWARE: PatentedSeq version 1.0
/ SEQ ID NO 19
/ LENGTH: 475
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-004-762-19
```

```
Alignment Scores:
Pred. No.: 8,076-33 Length: 475
Score: 453.00 Matches: 84
Percent Similarity: 73.9% Conservative: 35
Best Local Similarity: 52.2% Mismatches: 38
Query Match: 26.2% Indels: 4
DB: 12 Gaps: 3
```

US-10-768-566-1 (1-317) x US-11-004-762-19 (1-475)

```
QY 131 ValArgAlaGlyCysValaProLeuMetGluAlaTyrGlyPheProTrrProGluMetLeu 150
DB 2 GGGCGGAGCTCGGCGAGCGGCGATGATGCTTCTTACGCGCGGAGATGCTC 61
QY 151 HisCysHisIlePhePheProLeuAbaPheAbaPheCysIleAlaValaGlnPheGlyHis--- 169
DB 62 AATGTGACAAAGTTCC---GAGGCGACGTGTGATGCGCATGACCCCGCCCAATGCC 118
QY 170 LeuProAlaThrAlaProProValAlaThrIleCysAlaGlnCysGluMetGluHisSer 189
DB 119 ACCGAAGCTCTCGAAGCCCAAGGATACAGTGTGCTCCGCTGTACAAAGATTGAA 178
QY 190 AlaAerGlyLeuMetGluGlnMetCysSerSerSerPheValValIlyMetArgIleIys 209
DB 179 TCGGAGGACCATCATCAACATCTGTGTGACAGGAGCTTGGCGTGAATGAAATCAAA 238
QY 210 GluIleIysIleGluIleGlnGlyAbaPheArgIleLeuIleGlyAlaGlnIlyIlyIlyIlyLeu 229
DB 239 GAAGTAAAGAAAGAAACGGTACAGAAAGATTGTC-----CCCAAGAAAGAAAGAACCC 292
QY 230 LeuIlyPheGlyProLeuIlyAbaPheArgIleAbaPheArgIleValLeuHisMetIysAan 249
DB 293 TTGAAGCTGGGGCCCATCAAGAAAGAGCTGAAGCGGCTGTCTTTCTTCTTAAAGAAAT 352
QY 250 GlyAlaGlyCysProCysProGlnLeuAbaPheSerLeuAlaGlySerPheLeuValMetGly 269
DB 353 GGGCGGAGCTGTCCCTGCGACCAAGCTGACCAACTTCCATCATCATGAGG 412
QY 270 ArgIlyValaIspolYgInleuLeuMetAlaValIlyArgIlyAbaPheIlyIlyAbaPhe 289
DB 413 CCGAAGGTGAAGAGCCAGTACTTGTCTCAAGCCATTCAAGTGGAGCAAGAAAGAAAG 472
```

```
QY 290 Glu 290
DB 473 GAG 475
```

RESULT 8

```
US-09-925-065A-68204
/ Sequence 68204, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108627.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 68204
/ LENGTH: 631
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-68204
```

```
Alignment Scores:
Pred. No.: 6,636-31 Length: 631
Score: 434.00 Matches: 115
Percent Similarity: 52.8% Conservative: 15
Best Local Similarity: 46.7% Mismatches: 65
Query Match: 25.1% Indels: 52
DB: 6 Gaps: 6
```

US-10-768-566-1 (1-317) x US-09-925-065A-68204 (1-631)

```
QY 56 IleProAlaAerPheProLeuCysHisThrValGlyTyrIlyAbaPheArgIleProAan 75
DB 2 CTTCGAAGAGCGGCGCCCAAGTGCATGCATGCTTATCCCTCTCGGGAGGCCAC 60
QY 76 LeuLeuGluHisGluSerLeuAlaGluValIlyGlnAlaIleSerSerTrpLeuProLeu 95
DB 61 ATGCTGCTCCATCAAGAGCTC-----TTCACCCCTGCTTGG 96
QY 96 LeuAlaIlyAbaPheCysHisSerAbaPheArgIleValPheLeuCysSerLeuPheAlaProVal 115
DB 97 GTC-----TTCGAAGAGGCTTGGACTTCGATTCAAGCAGATC 135
QY 116 CysLeuAbaPheProIleTyrPro-----Cys 124
DB 136 ACAAGCTCTTCAAGCCCTCAATTCCTCTGTGACTTGAAGATGAAGATGATGCTGT 195
QY 125 ArgSerLeuCysGluAlaValaIlyAlaIly-----CysAlaProLeuMetGlu 140
DB 196 CTTGAGAGTCAAGCATGATAGTCTTCAATTAATGAAATGTGCC-----CTAGA 249
QY 141 AlaTyrGlyPheProTrrProGluMetLeuHisCysHisIlyIlyPhePheLeuAbaPhe 160
DB 250 GCTTCACCTTTCAGAGCCCGGAGGCGATC----- 279
QY 161 LeuCysIleAlaValaGlnPheGlyHisLeuProAlaThrAlaProProValThrIlyIle 180
DB 280 -----AGGCTCCCGCAGCCGCAAGGTCCAGAACACACCAAC 315
QY 181 CysAlaGlnCysGluMetGluHisSerAlaAbaPheIlyLeuMetGluGlnMetCysSerSer 200
```

[illegible]

Db	1057	GACCATGAAGAGGTGTGAGCAGCAGCCGGCGCTTGATCCCGCTGCATGAAGCAGTG	1116
Qy	100	ehiSerAspThrGlnValPheLeuCySerLeuPheAlaProValCys-----Le	117
Db	1117	CCACCCGGACACCAAGAGTTCCTGTCTCTGCTCTTGCGCCCGCTGCTCGATGACCT	1176
Qy	117	uAspArgProIleTyrProCySarGSerLeuCyGluValAlaTrpAlaGlyCysAlaPr	137
Db	1177	AGACGAGACCATTCAGCCATATCCACTGCTTGGCTGTGACAGGTGAAGACCGCTGCGCCC	1236
Qy	137	oLeuMetGluValaTyrGlyPheProTyrProGluMetLeuHiAcCysHiAluSrpPheProLe	157
Db	1237	GGTATGTCGCGCTTCGCGCTTCGCCCTGCGCCGACATGCTTGAATGCGCAGCGTTTCCCCCA	1296
Qy	157	uAspAsnAspLeuCySillAlaValAlaGlnPheGlyHis-----LeuProAlaThr-----	173
Db	1297	GGACACACGACCTTGTGATCCCTCCCTGCTAGACGACCACTCTGTGCACGACCAACGAGA	1356
Qy	174	-----AlaProProValTh	178
Db	1357	AGTAAAGCCTTCCCTCTTGCTCCCACTCCCTGCTGCGCTGAGACGCTCCAGAGATC	1416
Qy	178	rIlysiIeCys-----AlaGlnCys	184
Db	1417	CCGCCCTGCGACGACGATCCAGATGCTC	1441
RESULT 10			
US-11-184-005-23			
; Sequence 23, Application US/11184005			
; Publication No. US20050256052A1			
GENERAL INFORMATION:			
APPLICANT: Luyten, Frank P.			
APPLICANT: Moos, Malcolm JR.			
APPLICANT: Hoang, Bang			
APPLICANT: Wang, Shouwen			
TITLE OF INVENTION: METHOD OF MODULATING TISSUE			
TITLE OF INVENTION: GROWTH USING FRZB PROTEIN			
FILE REFERENCE: NIH133.ICPC3			
CURRENT APPLICATION NUMBER: US/11/184, 005			
CURRENT FILING DATE: 2005-07-18			
PRIOR APPLICATION NUMBER: US 10/028051			
PRIOR FILING DATE: 2001-12-19			
PRIOR APPLICATION NUMBER: US 08/822333			
PRIOR FILING DATE: 1997-03-20			
PRIOR APPLICATION NUMBER: US 08/729, 452			
PRIOR FILING DATE: 1996-10-11			
NUMBER OF SEQ ID NOS: 23			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 23			
LENGTH: 1291			
TYPE: DNA			
ORGANISM: Xenopus laevis			
US-11-184-005-23			
Alignment Scores:			
Pred. No.: 1.16e-16 Length: 1291			
Score: 285.00 Matches: 76			
Percent Similarity: 46.2% Conservative: 50			
Best Local Similarity: 27.8% Mismatches: 93			
Query Match: 16.5% Indels: 54			
DB: 12 Gaps: 11			
US-10-768-566-1 (1-317) x US-11-184-005-23 (1-1291)			
Qy	57	ProhlaAspLeuProAlaCysHisThrValGlyTyrTyrAspArgMetArgLeuProAsnLeu	76
Db	178	CTGTGCGAGATTCACATGTGCAATCTATGTCATGAACTGACCAAGATGCCAACCAT	237
Qy	77	LeuGluHisGluSerLeuAlaGluValAlaGlnGlnAlaSerSerTyrLeuProLeuLeu	96
Db	238	CTCCACCAACGACACTCAAGCAATGATTCATCTGCGCAATTGAACAGTTTGAAGGTTTGCTG	297
Qy	97	AlaIlyAspArgCysHisSerAspThrGlnValPheLeuCySerLeuPheAlaProValCys	116

```

Db      298 ACCACTGAATGATGACGAGACCTTTTGTCTTTCTGTGTGACCATGTATCCCCCATTTGT 357
      117 Leu-----AapArpProLleTyrProCyAArgSerLeuCyAgluaValaValArg 132
      358 ACCATCGATTTTCCAGATGATACCAATTAAAGCTTGTGAAGTCCGTGTGCCAAAGGCCAG 417
      133 AAGAGTCyAAlaPProLeuMetGluAlaTyrglyPheProTyrProGluMetLeuHisCyA 152
      418 GCCGGCTGTGAGCCCTTCATTAAGTACCGGCACACTTGGCCAGAGAGCTGGCATGT 477
      153 HisLysPheProLeu---AapAnaPLeuCyAAlaValaGlnHe-----167
      478 GAAGAGCTGCCGTATATGACAGAGAGTGTGATCTCCCAAGGCTATCTGCACAGTG 537
      168 -----GlyHisLeuPro 171
      538 GAACAAAGAACAGATTCAATGCCAGACTTCCCATGGATTCAAAACAATGGAAATTCGCGA 597
      172 AAlaThrAlaProProValThrTyrlCyAAlaGlnCyAgluMetGluHisSerAlaAap 191
      598 AACACGGCA-----GATGACACTGTAAATGCAAGCCCATGAAGCTTCCCAAAAG 648
      192 GlyLeuMetGluGlnMetCySerSerAapPheValValLysMetArgLleLysGluLe 211
      649 ACGTATCTCAAGAT-----AATTCAATTAATGATATCAGACAAAGTGAAGAGGTG 702
      212 LysIleGluAsnGlyAapArgLysLeuIleGlyAlaGlnLysLysLysLeuLeuLys 231
      703 AAAGTAAATGCCACAGACCGACACAGCAAT-----GTGAAATAAAGAGATTTCTCAAG 756
      232 ProGlyProLeuLys---ArgLysAapThrLysArgLeuValLeuHisMetLysAasnGly 250
      757 TCTTCCTCACTGAACATCTCTTAAGACACAGTGAACCTGAC-----ACCAAC 804
      251 AAGAGTCyAProCyAProGlnLeuAapSerLeuAlaGlySerPheLeuValMetGlyArg 270
      805 TCAGGCTGCTGTGTGCCCGCCAGCTGTGTGCC---AATGAGAAATCAATTAATGAGGCTAT 861
      271 Lys-----ValAapGlyGlnLeu-----276
      862 GAAGACAAAGAGGCTCCAGGCTTACTACTAGTGAAGAGATCTTGGCCCAAAATGAGAG 921
      277 -----LeuLeuMetAlaValTyraArgTyrAapLysLys 287
      922 GATGCTTGTCTTAAGAAAGTCAGCGCTGGGATCAAAAG 960

```

RESULT 11
 US-11-184-005-1
 / Sequence 1, Application US/11184005
 / Publication No. US20050256052A1
 / GENERAL INFORMATION:
 / APPLICANT: Luyten, Frank P.
 / APPLICANT: Moos, Malcolm JR.
 / APPLICANT: Hoang, Bang
 / APPLICANT: Wang, Shouwen
 / TITLE OF INVENTION: METHOD OF MODULATING TISSUE
 / TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
 / FILE REFERENCE: NIH133, 1CPG3
 / CURRENT APPLICATION NUMBER: US/11/184, 005
 / CURRENT FILING DATE: 2005-07-18
 / PRIOR APPLICATION NUMBER: US 10/028051
 / PRIOR FILING DATE: 2001-12-19
 / PRIOR APPLICATION NUMBER: US 08/822333
 / PRIOR FILING DATE: 1997-03-20
 / PRIOR APPLICATION NUMBER: US 08/729,452
 / PRIOR FILING DATE: 1996-10-11
 / NUMBER OF SEQ ID NOS: 23
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1
 / LENGTH: 2374
 / TYPE: DNA
 / ORGANISM: Bos taurus

```

US-11-184-005-1
Alignment Scores:
Pred. No.: 3,286-16
Score: 283.50
Percent Similarity: 41.54
Best Local Similarity: 26.14
Query Match: 16.44
DB: 12 Gaps: 11

US-10-768-566-1 (1-317) x US-11-184-005-1 (1-2374)
      2 ArgAlaAlaAlaAlaAlaGly-GlyValArgThrAlaAlaLeuAlaLeuLeuGlyAl 21
      276 CGGAGATGCTGCTGCTGCGCGCGCGGCTACTGCGCTGCGCTGCGCTGCGCTGCGCT 335
      21 AlauHisTrpAlaProAlaArgCyAgluGluTyraPheTyrglyTyrglnAlaGluPr 41
      336 GCCCGAGCGCGCGCGCGCGCTGTGAG-----363
      41 OleuHisGlyArgSerTyrserysProProGlnCyALeuAapLleProAlaAapLeuPr 61
      364 -----CCGTTCCGATTC 377
      61 OleuCySHisThrValGlyTyrglyArgMetArgLeuProAanLeuLeuGluHisGluSe 81
      378 CCGTGTCAAGTCCCTGCGCCCTGGACATGATCAAGATGCCCAACCACTGTCAACAGAGC 437
      81 rLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeuAlaLysArgCyAHis 101
      438 CCAAGGCCAAGCCATCTCGGCCATGACAGAGTTCAAGATCTGCTGGGCAACCACTGCA 497
      101 sSerAapThrGlnValPheLeuCyAserSerLeuPheAlaProValCyALeu-----117
      498 CCGGATGCTGCTCTTCTCTGCTGTATGAGCGGCCATCTGCACATGACTTCCA 557
      118 -AapArpProLleTyrProCyAArgSerLeuCyAgluAlaValaAlaGlyCyAAlaPr 137
      558 GCACAGCCCAATCAAGCCCTGCACAGTCTGTGTGCGAGGGGCCCGCAGGGCTGTGAGGC 617
      137 OleuMetGluAlaTyrglyLysPheProTyrProGluMetLeuHisCyAHisLysPheProLe 157
      618 CATCTCATCAAGTACCGCCACTCGTGGCGGAAAGCTTGGCTCGAGAGCTCCAGT 677
      157 u---AapAnaPLeuCyAAlaValaGlnPheGlyHisLeuProAlaThrAlaProPr 176
      678 ATATGACCGCGCGCGTGTGATCTCCGAG-----GCCAT 713
      176 oValThrLysIleCyAAlaGlnCyAgluMetGluHisSer-----AlaAapGlyLe 193
      714 CGTCACTGCCGACGAGCGGATTTTCTATGATTCACATATGGAACCTGATGAGAGAGC 773
      193 uMetGluGlnMetCyA-----198
      774 AAGCAGTGAACGCTCAAAATGTAACCAAGTCAAGCTACACAGAAACCTATTTCCGAAA 833
      199 -sSerAapPheValValaLysMetArgLleLysGluLleLysIleGluAasnGlyAapAr 218
      834 CAATTACAACATATGCTATCGGCGGTAAAGTTAAATAAAGAACAGATGTCATGAT-- 891
      218 GlyLeuLleGlyAlaGlnLysLysLysLysLeuLeuLysProGlyProLeuLysArgLys 238
      892 ---GTGACTGCAAGTGAAGAGTGAAGAGATTTTAAAGGCTTCTGTGTA-----939
      238 sAapThrLysArgLeuValLeuHisMetLysAasnGlyAlaGlyCyAProCyAProGlnLe 258
      940 -AACATTCCAAGGAAAGTGAACCTTATACCAAGCTGTGCTGCTGTGCTGCTGCTGCT 998
      258 uAapSerLeuAlaGlySerPheLeuValMetGlyTyrglys-----271
      999 T---AACGTATATGAGAGTATCTATCATGTGGCTACAGAAAGTGAAGAGCGCTCCAGATT 1055
      272 -----ValAapGlyGlnLeu-----LeuLeuMetAlaValTy 282

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Db      1056 ACTGTGGTACGAAGCTTCTATTGCTCGAAGAAATGGAAGATCGACTTGGTAAAAAAAGTTAA 1115
Qy      282 TATGTTPASPLYSLSYSAENLYSGLUmet 291
Db      1116 GCGGTGGGATATGAAAGCTCCGCATCTT 1143

RESULT 12
US-11-054-281-35
; Sequence 35, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/11/054,281
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; -PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-054-281-35

Alignment Scores:
Pred. No.:      6,31e-16      Length:      2184
Score:          280.00      Matches:      68
Best Similarity: 50.6%      Conservative: 22
Best Local Similarity: 38.2%  Mismatches:   64
Query Match:    16.2%      Indels:      26
DB:             12          Gaps:          6

US-10-768-566-1 (1-317) x US-11-054-281-35 (1-2184)
Qy      5 ALaAlaAlaGlyGlyValArgThraAlaLeuAlaLeuLeuGlyAlaLeuHisTrp 24
      |||:::|||||
Db      37 GCCTTGGCGGGGGGGCGCTGCTGTGGCACTGCTGG-CGCGGGCGGCGCGGCATCG 95
Qy      25 AlaProAlaArgCysGluGluIuTrpAspTyrTyrGlyTrpGlnAlaGluProLeuHisGly 44
      |||:::|||||
Db      96 AGATC-GGCCCG-----TTGACCCCGAGCGCGG 124
Qy      45 ArgSerTyrSerLysProProGlnCysLeuAspIleProAlaAspLeuProLeuCysHis 64
      |||:::|||||
Db      125 CGCGGG--GCTGCCCGCTGCGCAGCGCGGTGGAGATC-----CCCATGTGCCGC 169
Qy      65 ThrValGlyTyrLysArgMetArgLeuProAlaLeuLeuGluHisGluSerLeuAlaGlu 84
      |||:::|||||
Db      170 GGCATCGGCTTAAACCTGACCCGCAATGCCCACTGCTGGGCGCAACGTCGCGAGCGAG 229
Qy      85 VallySGInGlnAlaSerSerTrpLeuProLeuLeuAlaAlaYsArgCysHisSerAspThr 104
      |||:::|||||
Db      230 GCGCGTCCGACGCTAGCGGAGTTCGCGCGCGCGTGGTGGCACTACGCGTGCACAGCACCTG 289
Qy      105 GlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArg-----ProIle 121
      |||:::|||||

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Db      290  CGGTTCTCTCTGTCGCTCGCTTCAAGCGCCCAATGTGCACCGACCGAAGTCTCGAGCCCATT 349
Oy      122  TyPrCYaTgSerLeuCYaGluAlaValAlTgAlaGlyCYaAlaProLeuMetGluAla 141
Db      350  CCGCGCTGCGCGCCCATGTGCAGACGAGCGCGCTGCGCGCTCGCGCCCATCATGTGACAG 409
Oy      142  TyGlyLPhEProTrpProGluMetLeuHISCYaSHISlyPheProLeuAaPaaAaP--- 160
Db      410  TTCACACTCGCGCTGCGCGGAGATCGCTGCACATGCGCGCGGCGCCACCGCGACGACCGG 469
Oy      161  -----LeuCYaIleAlaValGlnPheGlyHISLeuProAlaTrpAlaProPro 176
Db      470  CAGCGCTGTGCATGTGAGCGCGCGCCAGAAC-----GCCACGCGCGCGCC 514

RESULT 13
US-11-184-005-3
; Sequence 3, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Mang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
; FILE REFERENCE: NIHJ33.1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-184-005-3

Alignment Scores:
Pred. No.: 4,46e-16 Length: 1484
Score: 279.50 Matches: 85
Percent Similarity: 41.5% Conservative: 52
Best Local Similarity: 25.8% Mismatches: 113
Query Match: 16.2% Indels: 80
DB: 12 Gaps: 11

US-10-768-566-1 (1-317) x US-11-184-005-3 (1-1484)
Oy      2  ATGAAATAAATAAATAAGT-GTValArgThrAlaAlaLeuAlaLeuLeuGluAl 21
Db      228  AGGAATGCTGCTGCTGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCGGGT 287
Oy      21  aLeuHISLTrpAlaProAlaArgCYaGluGlnTyrAaPTrpGlyTrpGlnAlaGluPr 41
Db      288  GCCCGGCGCTGCGCGCGCGACGCGCTGTGAG----- 315
Oy      41  oLeuHISLArgSerTyrSerLysProProGlnCYaLeuAaPTrpAlaAaPLeuPr 61
Db      316  -----CCCGTCCGCAATCC 329
Oy      61  oLeuCYaHISLTrpValGlyTyrLysArgMetArgLeuProAaPLeuLeuGlnHISgluSe 81
Db      330  CCTGTGAAATGCTGCTGCTGCGGAAACATGATCTAAGATGCGCAACACCTGACACAGAC 388
Oy      81  rLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCYaH 102
Db      390  TCAAGGCAACGCGCATCTGCGCGCATGAGAGATGTCACAAAGTGTGCTGCGGCAACCACTG 449
Oy      101  sSerAaPTrpGlnValPheLeuCYaSerLeuPheAlaProValCYaLeu----- 117

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Db      450  CCCGATCTGCTCTTCTTCTCTCTGCGATGAGGCGCCATGTGACCAATTGACTTCCA 509
Qy      118  -AsparGProIleTyRProCyAArgSerLeuCyGluAlaValArgAlaGlyCyAlaIyr 137
Db      510  GGAAGAGCCCATTAAGCCCTGTATAGTCTGTGTGCGAGCGGCGCCGACAGGCTGTAGCC 569
Qy      137  oLeuMetGluAlaTyRgLyPheProTrpProGluMetLeuHisCyGHisIlePheProIle 157
Db      570  CATACTCATCAAGTACCGCCACTCGTGGCCGAGAACCTGGCCCTGCGAGAGCTGCCAGT 629
Qy      157  u---AspAsnArgLeuCyAlleAlaValAlaGlnPheGlyHisLeuProAlaThrIaProPr 176
Db      630  GTAACGACAGGCGCGGTGGATCTCTCCCGAG-----GCCAT 665
Qy      176  oValThrIyAlleCyAlaGlnCySerGluMetGluHisSer-----AlaAspIlyLe 193
Db      666  CGTTATGGGAGCGAGAGCTGATTTCTCTATGATTTCTAGTAAGGAAAGCTAGAGGGCG 725
Qy      193  uMetGluIleMetCys----- 198
Db      726  AAGCACTGAACGCTGTAAATGTAGCCCTATTAGACTACACAGAACCTATTCCGGA 785
Qy      199  -SerSerAspPheValValIleMetArgIleIySerGluIleIyValIleGluAsnGlyAspAr 218
Db      786  CAATTACAACTATGTATTGCGGCTAAAGTTAAAGATTAAGACTTAAGTGCCTATAT-- 843
Qy      218  gLySerIleIleGlyAlaGlnIleIySerIleIySerIleIySerProGlyProIleIySerIy 238
Db      844  ----GTGACTGCGAGTGTGAGGTGAAGAGATTCTTAAGTCTCTCTGTGTA----- 891
Qy      238  sAspThrIyIyArgLeuValIleuHisMetIyAsnGlyAlaGlyCyAsProCyAsProIle 258
Db      892  -AACATTCACAGCGGACACTGTCAACCTTATACAGCTGTGGCTGCTGCGCTCCACT 950
Qy      258  uAspSerIleuAlaGlySerPheLeuValMetGlyArgIyS----- 271
Db      951  T---AATGTTAATGAGAAATATATATCATGAGGCTATGAAGATGAGAAAGTTCCAGATT 1007
Qy      272  -----ValAspGlyGlnLeu-----LeuLeuMetAlaValIyr 282
Db      1008  ACTCTTGCTGAGAGGCTCTATATAGCTGAGAAGTGAAGATCGACTCGTAAAAAAGTTAA 1067
Qy      282  rArgTrpAspIyIyIyAsnIySerGluMet 291
Db      1068  GCGCTGGATATGAGCTTCGTACTCTT 1095

RESULT 14
US-11-127-877-26
; Sequence 26, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merck, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitznagel, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Method, Compositions and Compound Assays for Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127, 877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-26

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```

Alignment Scores:
Pred. No.: 1,796-15
Score: 276.00
Percent Similarity: 52.14
Best Local Similarity: 37.11
Query Match: 16.04
DB: 12 Gaps: 6

US-10-768-566-1 (1-317) x US-11-127-877-26 (1-2561)
Qy      19  LeuGlyAlaLeuHisThrAlaProAlaArgCyGluGluIyTyAspTrpTyRgIyTrpGln 38
Db      390  CTCGGCTGATCCCATCCGCGCGCCCTGCTTGTGTGTCTGTCTGCGAGAGCTGTGG 449
Qy      39  AlaGluProLeuHisGlyArg--SerTySerIySerProGluIyCyLeuAspIleProA 58
Db      450  GCC-----GGGCGCGCGCGCGCTCCAAAGCCCGGTGTGCCAGGAATC----- 493
Qy      58  lAspLeuProLeuCyHisIleThrValGlyTyRgIyArgMetArgLeuProAlaLeuG 78
Db      494  --ACGGTGCCTATGTGCGCGCGCATCGCTACAACTGACGACATGCCCAACAGTTCA 551
Qy      78  lHisGluSerLeuAlaGluValIyGlnAlaIleSerSerTrpLeuProLeuAlaI 98
Db      552  ACCACGACACGACGACGAGCGCGCGCTGAGAGTCAACAGTTCTGCGCGCTGTGGAGA 611
Qy      98  yArgCyHisSerAspThrGlnValPheLeuCySerIlePheAlaProValCyLeu- 117
Db      612  TCCATGTCTGCGCGGACCGGCTTCTCTATGTCTATGTATGACAGCGCCATCTGTGCG 671
Qy      118  -----AspArgProIleTyRProCyArgSerLeuCyGluAlaValArgAlaGlyC 135
Db      672  CCGACTACCAAGCGCGCTGCGCGCTGCGCTGCGTGTGTGCGAGCGCGCAAGCGCGCT 731
Qy      135  yAlaProLeuMetGluAlaTyRgIyPheProTrpProGluMetLeuHisCyHisIlySP 155
Db      732  GCTGCGCTGATGTGCGCGCATGAGCTGTGCGCTGCGCGCGAGCGCATGAGCTGCGCGCT 791
Qy      155  hePro--LeuAspAsnSP-----LeuCyAlaAlaValAlaGlnPheGlyHisIlySP 171
Db      792  TCCCGGTGCTGGCGCGGACGCGCGAGTCTGTGATGATTAACAACGCGAGGAG---G 848
Qy      171  rAlaIleThrAlaProPro 176
Db      849  CCACCAAGCGCGCGCGCC 865

RESULT 15
US-11-067-231-154
; Sequence 154, Application US/11067231
; Publication No. US20050272063A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yousuke
; APPLICANT: Katagiri, Toyomasa
; APPLICANT: Fukukawa, Chikako
; TITLE OF INVENTION: METHOD FOR TREATING SYNOVIAL SARCOMA
; FILE REFERENCE: 1254-0272PUS1
; CURRENT APPLICATION NUMBER: US/11/067,231
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/407,506
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/486,195
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/JP03/10591
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: PCT/JP2004/002144
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US 60/598,834
; PRIOR FILING DATE: 2004-08-05
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 2811
; TYPE: DNA

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 22, 2006, 22:42:32 ; Search time 47 Seconds
(without alignments)
557.621 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730
Sequence: 1 MRAAAGVTRTALALTLG.....MFSYPSLYPPFYGNAPPH 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCtus_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1730	100.0	317	2	US-08-937-067-6 Sequence 6, Appli
2	1730	100.0	317	2	US-09-949-016-6300 Sequence 6300, Ap
3	1674	96.8	305	2	US-09-949-016-7706 Sequence 7706, Ap
4	924.5	53.4	314	2	US-08-937-067-7 Sequence 7, Appli
5	917	53.0	313	2	US-09-546-043-3 Sequence 3, Appli
6	917	53.0	338	2	US-09-546-043-4 Sequence 4, Appli
7	915	52.9	313	2	US-09-514-885-1 Sequence 1, Appli
8	915	52.9	313	2	US-09-949-016-6299 Sequence 6299, Ap
9	869.5	50.3	314	2	US-09-087-031E-3 Sequence 1, Appli
10	860	49.7	313	2	US-09-087-031E-4 Sequence 4, Appli
11	714	41.3	267	2	US-09-546-043-7 Sequence 7, Appli
12	659	38.1	246	2	US-09-546-043-6 Sequence 6, Appli
13	617.5	35.7	295	2	US-08-937-067-2 Sequence 2, Appli
14	610.5	35.3	295	2	US-09-999-833A-415 Sequence 415, App
15	610.5	35.3	295	2	US-10-020-445A-415 Sequence 415, App
16	609	35.2	295	2	US-09-148-545-179 Sequence 179, App
17	609	35.2	295	2	US-09-621-011-179 Sequence 179, App
18	609	35.2	296	2	US-09-148-545-237 Sequence 237, App
19	609	35.2	296	2	US-09-621-011-237 Sequence 237, App
20	564.5	32.6	295	2	US-08-893-654B-6 Sequence 6, Appli
21	555.5	32.1	195	2	US-09-546-043-5 Sequence 5, Appli
22	475.5	27.5	212	2	US-08-937-067-4 Sequence 4, Appli
23	442.5	25.6	109	2	US-09-087-031E-19 Sequence 19, Appli
24	401.5	23.2	229	2	US-09-546-043-8 Sequence 8, Appli
25	398	23.0	280	2	US-08-893-654B-4 Sequence 4, Appli
26	381.5	22.1	113	2	US-09-087-031E-24 Sequence 24, Appli
27	372.5	21.5	281	2	US-08-893-654B-2 Sequence 2, Appli

28	285	16.5	319	2	US-10-028-051A-7 Sequence 7, Appli
29	284.5	16.4	572	2	US-08-937-067-13 Sequence 13, Appli
30	283.5	16.4	318	2	US-08-878-474-3 Sequence 3, Appli
31	283	16.4	319	2	US-10-014-055-7 Sequence 7, Appli
32	279	16.1	318	2	US-10-014-055-8 Sequence 8, Appli
33	279	16.1	325	2	US-10-014-055-2 Sequence 2, Appli
34	276.5	16.1	325	2	US-10-028-051A-2 Sequence 2, Appli
35	276.5	16.0	319	2	US-10-028-051A-8 Sequence 8, Appli
36	275	15.9	325	2	US-08-878-474-9 Sequence 9, Appli
37	275	15.9	325	2	US-09-976-594-479 Sequence 479, App
38	275	15.9	325	2	US-10-014-055-4 Sequence 4, Appli
39	275	15.9	325	2	US-10-028-051A-4 Sequence 4, Appli
40	275	15.9	371	2	US-09-949-016-7544 Sequence 7544, Ap
41	272	15.7	323	2	US-08-878-474-7 Sequence 7, Appli
42	270	15.6	585	2	US-08-937-067-9 Sequence 9, Appli
43	263.5	15.2	685	2	US-08-937-067-14 Sequence 14, Appli
44	262.5	15.2	565	2	US-08-937-067-8 Sequence 8, Appli
45	252.5	14.6	111	2	US-10-014-055-6 Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-08-937-067-6
/ Sequence 6, Application US/08937067
/ Patent No. 6433155
/ GENERAL INFORMATION:
/ APPLICANT: Unanaky, Samuel
/ TITLE OF INVENTION: A FAMILY OF GENES ENCODING
/ TITLE OF INVENTION: ADOPTIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
/ TITLE OF INVENTION: METHODS OF USE THEREOF
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: MORRISON & FOERSTER
/ STREET: 755 Page Mill Road
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/937, 067
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lehnhardt, Susan K.
/ REGISTRATION NUMBER: 33,943
/ REFERENCE/DOCKET NUMBER: 23647-20018, 00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 813-5600
/ TELEFAX: (650) 494-0792
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-937-067-6
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Query Match 100.0%; Score 1730; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.3e-193;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAAAGVTRTALALTLGALHWAPARCEVDYGGQAEPLHGRSVSKPPQCLDIPDL 60
DB 1 MRAAAGVTRTALALTLGALHWAPARCEVDYGGQAEPLHGRSVSKPPQCLDIPDL 60
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QY 61 PLCHTVGYKRMRLPNLLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRP 120
Db 61 PLCHTVGYKRMRLPNLLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRP 120
QY 121 IYPCSLCEAVAGACAPLMEAYGFPMPPEMLHCHKPFLDNDLCIAVOFGHLPTATAPVTKI 180
Db 121 IYPCSLCEAVAGACAPLMEAYGFPMPPEMLHCHKPFLDNDLCIAVOFGHLPTATAPVTKI 180
QY 181 CAOCMEHSADGLMEOWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPKRKYD 240
Db 181 CAOCMEHSADGLMEOWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPKRKYD 240
QY 241 KRLVLMKNGAGACPCPOLDSLGSFLVMGRKVDGQLLLMAVYRMDKXKMKFAVKFMS 300
Db 241 KRLVLMKNGAGACPCPOLDSLGSFLVMGRKVDGQLLLMAVYRMDKXKMKFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
Db 301 YPCSLYYPFFYGAAEPH 317

RESULT 2
US-09-949-016-6300
; Sequence 6300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,766
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6300
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6300

Query Match 100.0%; Score 1730; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.3e-193;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-949-016-7706
; Sequence 7706, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,766
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7706
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7706

Query Match 96.8%; Score 1674; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.1e-186;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 13 AALALLGALHMAPRCEEDYDYGQAEPLHGRSYPQCLDIPADLPCHTVGYKMR 72
Db 1 AALALLGALHMAPRCEEDYDYGQAEPLHGRSYPQCLDIPADLPCHTVGYKMR 60
QY 73 LPNLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRPFCRSICEAVR 132
Db 61 LPNLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRPFCRSICEAVR 120
QY 133 AGCAPLMEAYGFPMPPEMLHCHKPFLDNDLCIAVOFGHLPTATAPVTKICAOCMEHSADG 192
Db 121 AGCAPLMEAYGFPMPPEMLHCHKPFLDNDLCIAVOFGHLPTATAPVTKICAOCMEHSADG 180
QY 181 LMEQWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPKRKYDRLVLMKNGAG 252
Db 181 LMEQWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPKRKYDRLVLMKNGAG 240
QY 253 CPCPOLDSLGSFLVMGRKVDGQLLLMAVYRMDKXKMKFAVKFMSYPCSLYYPFFYG 312
Db 241 CPCPOLDSLGSFLVMGRKVDGQLLLMAVYRMDKXKMKFAVKFMSYPCSLYYPFFYG 300
QY 313 AAEPH 317
Db 301 AAEPH 305

RESULT 4
US-08-937-067-7
; Sequence 7, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umaneky, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-937-067-7

Query Match 53.4%; Score 924.5; DB 2; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.8e-99;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGGVTALAL--LGLHWPAPRCEVDYGMQAE--PLH-GRSYSKPQCLD 55
DB 1 MGIGSEGRGAGLGVLLALGALLAVGASAEYDVVSQSDIGPQSRFTKPPQCD 60
QY 56 IPADPLCTTGYKRLNLLHESLAIVKQOASSWPLAKRCHSDTOVFLCSFPAV 115
DB 61 IPADRLCHNAGVKKRVLLNLEHETMAEVKQOASSWVPLNKNCHAGQVFLCSLFAV 120
QY 116 CDRPIYPCRSICEAVRAGCAPLMEAYGFPWPEMLHCHFPDLNDLCTIAVQGH--LPATA 174
DB 121 CDRPIYPCRWLCEAVRDCSEVWQFPGFYWPEMLKCDKFP--EGVVCIAMTPPNPTASK 179
QY 175 PVTYKICAOCEMEHSADGLMEQSSDFVVKRIKIKIENGDRKLGAQKKKLLKPGP 234
DB 180 PGCTTCPCPCDNELKSEALIEHLCASEFALRMKIKEVKENGDKKIV--PKKKKPLKLG 237
QY 235 LKRKDTKRLVLAHKNAGCPCCPOLDSLASFVLMGRKVDGOLLMAVYRMDKKNEMKKA 294
DB 238 IKKKDLKKLVLYLKNAGDCPCQOLDNLSHHFLIMGRKVSQYLLTAIHKMDKKNEFKNF 297
QY 295 VKFMFSPCSLYYPPF 310
DB 298 MKKMKNECPFOSVF 313

RESULT 5
US-09-546-043-3
Sequence 3, Application US/09546043
Patent No. 6600018
GENERAL INFORMATION:
APPLICANT: Rubin, Jeffery et al.,
TITLE OF INVENTION: SECRETED FRITZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
FILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 53990
CURRENT APPLICATION NUMBER: US/09/546,043
CURRENT FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 3
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-546-043-3

Query Match 53.0%; Score 917; DB 2; Length 313;
Best Local Similarity 57.9%; Pred. No. 2.8e-98;
Matches 179; Conservative 50; Mismatches 70; Indels 10; Gaps 7;

QY 8 GGVTAALALLIGALHWPAP--CEVDYGMQAE--PLH-GRSYSKPQCLDIPADPL 62
DB 8 GGRGAGLGVLL--ALGASGRGLGSEYDVVSFQSDIGPQSRFTKPPQCDVIPADRL 66
QY 63 CHTVGKRMRLPNLLEHESLAIVKQOASSWPLAKRCHSDTOVFLCSLFAVPCDRPIY 122
DB 67 CHNVGKRMVLPNLEHETMAEVKQOASSWVPLNKNCHAGTOVFLCSLFAVPCDRPIY 126
QY 123 PCSICEAVRAGCAPLMEAYGFPWPEMLHCHFPDLNDLCTIAVQGH--LPATAPVTYKIC 181
DB 127 PCRWLCEAVRDCSEVWQFPGFYWPEMLKCDKFP--EGVVCIAMTPPNPTASKPGCTTVC 185
QY 182 AOCMEHSADGLMEQSSDFVVKRIKIKIENGDRKLGAQKKKLLKPGPLKRDYK 241
DB 186 PCDNELKSEALIEHLCASEFALRMKIKEVKENGDKKIV--PKKKKPLKLGPIKKDLK 243
QY 242 RLVIHMKRAGCPCCPOLDSLASFVLMGRKVDGOLLMAVYRMDKKNEMKFAVFMFSP 301
DB 244 KLVLYLKNAGDCPCQOLDNLSHHFLIMGRKVSQYLLTAIHKMDKKNEFKNFKMKNH 303
QY 302 PCSLYYPPF 310
DB 304 ECPFOSVF 312

RESULT 6
US-09-546-043-4
Sequence 4, Application US/09546043
Patent No. 6600018
GENERAL INFORMATION:
APPLICANT: Rubin, Jeffery et al.,
TITLE OF INVENTION: SECRETED FRITZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
FILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 53990
CURRENT APPLICATION NUMBER: US/09/546,043
CURRENT FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 4
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-546-043-4

Query Match 53.0%; Score 917; DB 2; Length 338;
Best Local Similarity 57.9%; Pred. No. 3.2e-98;
Matches 179; Conservative 50; Mismatches 70; Indels 10; Gaps 7;

QY 8 GGVTAALALLIGALHWPAP--CEVDYGMQAE--PLH-GRSYSKPQCLDIPADPL 62
DB 8 GGRGAGLGVLL--ALGASGRGLGSEYDVVSFQSDIGPQSRFTKPPQCDVIPADRL 66
QY 63 CHTVGKRMRLPNLLEHESLAIVKQOASSWPLAKRCHSDTOVFLCSLFAVPCDRPIY 122
DB 67 CHNVGKRMVLPNLEHETMAEVKQOASSWVPLNKNCHAGTOVFLCSLFAVPCDRPIY 126
QY 123 PCSICEAVRAGCAPLMEAYGFPWPEMLHCHFPDLNDLCTIAVQGH--LPATAPVTYKIC 181
DB 127 PCRWLCEAVRDCSEVWQFPGFYWPEMLKCDKFP--EGVVCIAMTPPNPTASKPGCTTVC 185
QY 182 AOCMEHSADGLMEQSSDFVVKRIKIKIENGDRKLGAQKKKLLKPGPLKRDYK 241
DB 186 PCDNELKSEALIEHLCASEFALRMKIKEVKENGDKKIV--PKKKKPLKLGPIKKDLK 243
QY 242 RLVIHMKRAGCPCCPOLDSLASFVLMGRKVDGOLLMAVYRMDKKNEMKFAVFMFSP 301
DB 244 KLVLYLKNAGDCPCQOLDNLSHHFLIMGRKVSQYLLTAIHKMDKKNEFKNFKMKNH 303
QY 302 PCSLYYPPF 310

Db 121 CUDRPIYPCRMICEAVRDSCEPVMGFFGYWPEMLKCDKRP-EGDVCIAMTPPNATEASK 179
Qy 175 PAVTKICAOCMEHSDAGLMEQSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPP 234
Db 180 PGTTVCPCPDNLKSEBAIIENHCASEFALRMKIKEYKKNENDKITV--PKKKKPLKGP 237
Qy 235 LRRKDTKRLVLMKNGAGCPCPOLDSLAGSFLVMGKRVQDQLLMAVYRMDKKXKEMKA 294
Db 238 IKKDKLKKIYLVLMKNGADCFCHGLDNLSHHFLIMGRKRVSGYLLTAIHKKMDKKKKEFKNF 297
Qy 295 VKEMFSPCSLYYPPF 310
Db 298 MKMKMHCEPTFGSVF 313

RESULT 10
US-09-087-031E-4
; Sequence 4, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-4

Query Match 49.7%; Score 860; DB 2; Length 313;
Best Local Similarity 54.3%; Pred. No. 1.3e-91;
Matches 171; Conservative 48; Mismatches 88; Indels 8; Gaps 6;
Qy 1 MRAAAGGCTA-ATALLGALHMAPRCEYDY--YGMQAEPL-HGRSYKPPQCLDI 56
Db 1 MGIAGSEGRKGLVLLALGALLAVGSASEYDVSFGSDIGFYGSGRFTKPPGCVDI 60
Qy 57 PADLPLCHTVGYKRMRLPNLLEHESLAEVKQOASSWPLAKRCHSDTOVFLCSLFAVPC 116
Db 61 PADLRLCHNVGYKRMVLPNLEHETMAEVKGGASSWVPLLNKCHAGTGVFLCSLFAVPC 120
Qy 117 LDRPIYPCSLCBAYVAGCAPLMEAYGFPWPEMLHCHKRPDLNDLCIAVOFGH-LPATAP 175
Db 121 LDRPIYPCSMLEAYVADSCEPVMGFFGYWPEMLKCDKRP-EGDVCIAMTPPNATEASK 179
Qy 176 PVTKICAOCMEHSDAGLMEQSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPPGL 235
Db 180 PGTTVCPCPDNLKSEBAIIENHCASEFALRMKIKEYKKNENDKITV--PKKKKPLKGP 237
Qy 236 KRRDTRKRLVLMKNGAGCPCPOLDSLAGSFLVMGKRVQDQLLMAVYRMDKKXKEMKFAV 295
Db 238 KKKDKLKKIYLVLMKNGADCFCHGLDNLSHHFLIMGRKRVSGYLLTAIHKKMDKKKKEFKNF 297
Qy 296 VKEMFSPCSLYYPPF 310
Db 298 MKMKMHCEPTFGSVF 312

RESULT 11
US-09-546-043-7
; Sequence 7, Application US/09546043
; Patent No. 6600018

; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey et al.,
; TITLE OF INVENTION: SECRETED FRITZLED RELATED PROTEIN, SRP, FRAGMENTS AND
; FILE REFERENCE: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-7

Query Match 41.3%; Score 714; DB 2; Length 267;
Best Local Similarity 58.4%; Pred. No. 1.1e-74;
Matches 142; Conservative 38; Mismatches 53; Indels 10; Gaps 7;
Qy 8 GGVTAALALLGALHMAPR--CEEYDYGMQAE--PLH-GRSYKPPQCLDI PADLPL 62
Db 8 GGRGALLGVLL-ALGASGRGLSEYDYVSFGSDIGFYGSGRFTKPPGCVDI PADLRL 66
Qy 63 CHTVGYKRMRLPNLLEHESLAEVKQOASSWPLAKRCHSDTOVFLCSLFAVPCIDRPIY 122
Db 67 CHNVGYKRMVLPNLEHETMAEVKQOASSWVPLLNKCHAGTGVFLCSLFAVPCIDRPIY 126
Qy 123 PCSLCEAVRAGCAPLMEAYGFPWPEMLHCHKRPDLNDLCIAVOFGH-LPATAPVTKIC 181
Db 127 PCRMICEAVRDSCEPVMGFFGYWPEMLKCDKRP-EGDVCIAMTPPNATEASKPGTTVC 185
Qy 182 AQCEMEHSDAGLMEQSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPPLRKDKT 241
Db 186 PCDNELKSEBAIIENHCASEFALRMKIKEYKKNENDKITV--PKKKKPLKGP IKKDQ 243
Qy 242 RLV 244
Db 244 AYV 246

RESULT 12
US-09-546-043-6
; Sequence 6, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey et al.,
; TITLE OF INVENTION: SECRETED FRITZLED RELATED PROTEIN, SRP, FRAGMENTS AND
; FILE REFERENCE: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-6

Query Match 38.1%; Score 659; DB 2; Length 246;
Best Local Similarity 57.6%; Pred. No. 2.7e-68;
Matches 132; Conservative 36; Mismatches 49; Indels 12; Gaps 7;
Qy 8 GGVTAALALLGALHMAPR--CEEYDYGMQAE--PLH-GRSYKPPQCLDI PADLPL 62
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Qy 63 CHTVGYKRMRLPNLLEHESLAEVKQOASSWPLAKRCHSDTOVFLCSLFAVPCIDRPIY 122
Db 67 CHNVGYKRMVLPNLEHETMAEVKQOASSWVPLLNKCHAGTGVFLCSLFAVPCIDRPIY 126
Qy 123 PCSLCEAVRAGCAPLMEAYGFPWPEMLHCHKRPDLNDLCIAVOFGH-LPATAPVTKIC 181

Db 127 PCRWLCEAVRDSCEPVMQFPGFYWPBMLKCDKP--EGDVCIAMTPBNATEASKPGQTTVC 185
QY 182 ACCEMEHSADGLMEQWSSDFVVKRKRIKIKIENGDRKLIQAQKKKL 230
Db 186 PCEDNLEKSEALIIHLCASEFALRMKIKIKVKKENGQ-----AYEQKLI 230

RESULT 13
US-08-937-067-2
Sequence 2, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umaneky, Samuel
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEROF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-2

Query Match 35.7%; Score 617.5; DB 2; Length 295;
Best Local Similarity 43.8%; Pred. No. 2.4e-63;
Matches 126; Conservative 52; Mismatches 93; Indels 17; Gaps 7;

QY 13 AALALLLGLHWAPRCSEYDYVGWQAEPLHGRSYSKRPPCCDIPADPLCHTVGYKKMR 72
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QY 73 LPNLEHESLAEVKKOQASMLPLAKRCHSDPVOVFLCSLFAVYC---LDRPIYPCRSICE 129
Db 60 LPNLEHETMKKEVLEQAGAMIFLVWKQCHPDTKKFLCSLFAVYCLDDLDDETQPCHSICV 119
QY 130 AVRACAPLMEAYGFPWPEMLHCHKFPLNDLCIAVOFGH--LPAT--APPYTKICAQCE 185
Db 120 QVKRCAPYMSAFGFWPMDLECDRFPQNDLCIPLASDHLPLATEAR---KYCEACK 176
QY 186 MEHSADG-LMEQWSSDFVVKRKRIKIKIENGDRKLIQAQKKKLKPEPLRKQDTKRLV 244
Db 177 TKNEDNDNDMETLCKRDKFALKVKEITYINRDTKILLETKSKITYKJNGVSRDLKSKSV 236
QY 245 LHMKNAGAGPCPOLDSLAGSFLVMGRKVGOLLLAAVYVRMDKKNEMK 292
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RESULT 14
US-09-999-833A-415
Sequence 415, Application US/09999833A
Patent No. 6916648
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P26301C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
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PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664


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1 PRIOR FILING DATE: 1998-04-23
2 PRIOR APPLICATION NUMBER: 60/083336
3 PRIOR FILING DATE: 1998-04-27
4 PRIOR APPLICATION NUMBER: 60/083322
5 PRIOR FILING DATE: 1998-04-28
6 PRIOR APPLICATION NUMBER: 60/083392
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14 PRIOR APPLICATION NUMBER: 60/083545
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16 PRIOR APPLICATION NUMBER: 60/083554
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20 PRIOR APPLICATION NUMBER: 60/083559
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24 PRIOR APPLICATION NUMBER: 60/083742
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29 PRIOR FILING DATE: 1998-05-06
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31 PRIOR FILING DATE: 1998-05-06
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34 PRIOR APPLICATION NUMBER: 60/084639
35 PRIOR FILING DATE: 1998-05-07
36 PRIOR APPLICATION NUMBER: 60/084640
37 PRIOR FILING DATE: 1998-05-07
38 PRIOR APPLICATION NUMBER: 60/084598
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50 PRIOR APPLICATION NUMBER: 60/085323
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52 PRIOR APPLICATION NUMBER: 60/085582
53 PRIOR FILING DATE: 1998-05-15
54 PRIOR APPLICATION NUMBER: 60/085700
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56 PRIOR APPLICATION NUMBER: 60/085689
57 PRIOR FILING DATE: 1998-05-15
58 PRIOR APPLICATION NUMBER: 60/085579
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63 PRIOR FILING DATE: 1998-05-15
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65 PRIOR FILING DATE: 1998-05-15
66 PRIOR APPLICATION NUMBER: 60/085697
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Db      7  SLULLFLASHCCIGSARGBLFG--QPDPSYKRSNCKP-----IPVNIQLCGHIEYQWRLL 60
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QY      131 VRACGAPLMEAYGFPPEWMLCHKRPPLNDLCIAVQFQH--LPAT--APPYTKIAQCEM 186
Db      121 VKORCAPVMSAGFPMPDMLECDRRFPQNDLCIPLASDHLLPMTBEAP---KYCEACNK 177
QY      187 EHSADG-LMEQWSSDFVYQVRIKIKIYLENGDKILGAQKKKLLKGLPKRYKQTKLYL 245
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QY      246 HMGNGAGCCPCPOLDSIAGSFLVMGKRVQGGILLMAVVRMDKGNEMK 292
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Search completed: March 22, 2006, 22:43:55
Job time : 48 secs

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	Best Local Similarity	43.6%;	Pred.	No.1.6e-62;	
	Matches 125; Conservative	50;	Mismatches	95;	Gaps 7;
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Db      7  SLULLFLASHCCIGSARGBLFG--QPDPSYKRSNCKP-----IPVNIQLCGHIEYQWRLL 60
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Db      61  PNLLGHRTKMEVLEQAGAMIPLVMQKCHPDTKKFCSIAFVCLDDDETTIQCHSLCVQ 120
QY      131 VRACGAPLMEAYGFPPEWMLCHKRPPLNDLCIAVQFQH--LPAT--APPYTKIAQCEM 186
Db      121 VKORCAPVMSAGFPMPDMLECDRRFPQNDLCIPLASDHLLPMTBEAP---KYCEACNK 177
QY      187 EHSADG-LMEQWSSDFVYQVRIKIKIYLENGDKILGAQKKKLLKGLPKRYKQTKLYL 245
Db      178 KNDNDMDIMETLCKNDFAIKIKYKSIITYINDTKIILETSKTIYKUNGSEBDLKRSVL 237
QY      246 HMGNGAGCCPCPOLDSIAGSFLVMGKRVQGGILLMAVVRMDKGNEMK 292
Db      238 WLKDSIQCTCEEMNDINAPFLVMGKQGGELVITSYKRWQKQGRBPK 284

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Search completed: March 22, 2006, 22:43:55
Job time : 48 secs

	Query Match	35.3%	Score 610.5;	DB 2;	Length 295;
	Best Local Similarity	43.6%;	Pred.	No.1.6e-62;	
	Matches 125; Conservative	50;	Mismatches	95;	Gaps 7;
Oy	14 ALALLGLHNAAPRCEBYDYWGQAELPHGRSYSPQCCLDIPADLPLCTGVGYKRRRL	73	:	: :	:: :
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 22:43:17 / Search time 165 Seconds
(without alignments)
802.739 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGCVRTALALLG.....MFSYPSLYPPFGAEPH 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1730	100.0	317	4	US-10-146-474-6 Sequence 6, Appl1
2	1730	100.0	317	4	US-10-338-604-2 Sequence 2, Appl1
3	1730	100.0	317	4	US-10-301-764-6 Sequence 6, Appl1
4	1730	100.0	317	5	US-10-768-566-1 Sequence 1, Appl1
5	1613	93.2	314	4	US-10-338-604-5 Sequence 5, Appl1
6	924.5	53.4	314	4	US-10-146-474-7 Sequence 7, Appl1
7	924.5	53.4	314	4	US-10-138-434A-3 Sequence 3, Appl1
8	924.5	53.4	314	4	US-10-101-764-7 Sequence 7, Appl1
9	924.5	53.4	314	4	US-10-666-851-2 Sequence 2, Appl1
10	924.5	53.4	314	4	US-10-788-792-148 Sequence 148, App
11	924.5	53.4	314	5	US-10-756-149-5611 Sequence 5611, Ap
12	917	53.0	313	4	US-10-425-586-3 Sequence 3, Appl1
13	917	53.0	313	4	US-10-425-586-3 Sequence 3, Appl1
14	917	53.0	338	4	US-10-425-586-4 Sequence 4, Appl1
15	917	53.0	338	4	US-10-425-586-4 Sequence 4, Appl1
16	915	52.9	313	3	US-09-796-008-2 Sequence 2, Appl1
17	915	52.9	313	4	US-10-138-434A-4 Sequence 4, Appl1
18	915	52.9	313	4	US-10-666-851-7 Sequence 7, Appl1
19	915	52.9	313	4	US-10-786-720-43 Sequence 43, Appl1
20	915	52.9	313	5	US-10-817-525-2 Sequence 2, Appl1
21	915	52.9	313	5	US-10-847-972-77 Sequence 77, Appl1
22	903	52.2	314	5	US-10-847-972-80 Sequence 80, Appl1
23	714	41.3	267	4	US-10-425-586-7 Sequence 7, Appl1
24	714	41.3	267	4	US-10-466-136-7 Sequence 6, Appl1
25	659	38.1	246	4	US-10-425-586-6 Sequence 6, Appl1
26	659	38.1	246	4	US-10-466-136-6 Sequence 6, Appl1
27	620.5	35.9	295	3	US-09-934-483A-1 Sequence 1, Appl1

28	620.5	35.9	295	3	US-09-934-483A-5	Sequence 5, Appl1
29	620.5	35.9	295	5	US-10-847-972-81	Sequence 81, Appl1
30	620.5	35.9	295	5	US-10-432-256-5	Sequence 5, Appl1
31	617.5	35.7	295	4	US-10-146-474-2	Sequence 2, Appl1
32	617.5	35.7	295	4	US-10-301-764-2	Sequence 2, Appl1
33	614.5	35.5	295	2	US-08-949-904-2	Sequence 2, Appl1
34	614.5	35.5	295	4	US-10-177-293-142	Sequence 142, App
35	614.5	35.5	295	4	US-10-295-027-1345	Sequence 1345, App
36	614.5	35.5	295	5	US-10-783-528-107	Sequence 107, App
37	614.5	35.5	295	5	US-10-847-972-78	Sequence 78, Appl1
38	614.5	35.5	295	5	US-10-432-256-2	Sequence 2, Appl1
39	614	35.5	275	2	US-08-949-904-3	Sequence 3, Appl1
40	610.5	35.3	295	3	US-09-978-295A-415	Sequence 415, App
41	610.5	35.3	295	3	US-09-978-697-415	Sequence 415, App
42	610.5	35.3	295	3	US-09-978-192A-415	Sequence 415, App
43	610.5	35.3	295	3	US-09-999-832A-415	Sequence 415, App
44	610.5	35.3	295	3	US-09-978-188-415	Sequence 415, App
45	610.5	35.3	295	3	US-09-978-608A-415	Sequence 415, App

ALIGNMENTS

RESULT 1
US-10-146-474-6
; Sequence 6, Application US/10146474
; Publication No. US20030023061A1
GENERAL INFORMATION:
APPLICANT: Umekanyan, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APPTOPSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-146-474-6
Query Match 100.0%; Score 1730; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRAAAGGVTAAATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPPQCLDIPADL 60
DB 1 MRAAAGGVTAAATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPPQCLDIPADL 60
QY 61 PLCHTVGKRMRLPULLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLPAVYCLDRP 120
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DB 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPATAPVTKI 180
QY 181 CAQCEMESHADGLMEQSSDFVVMRKIKIENGDRKLIQAOKKKKLLKPGPKRKYDT 240
DB 181 CAQCEMESHADGLMEQSSDFVVMRKIKIENGDRKLIQAOKKKKLLKPGPKRKYDT 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMFS 300
DB 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMFS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

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RESULT 2
US-10-338-604-2

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; Sequence 2, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; FILE REFERENCE: MP101-250P1RM
; CURRENT APPLICATION NUMBER: US/10/338,604
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-604-2

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Query Match 100.0%; Score 1730; DB 4; Length 317;

Best Local Similarity 100.0%; Pred. No. 4.6e-169; Indels 0; Gaps 0;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRAAAGGVTAAATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPPQCLDIPADL 60
QY 61 PLCHTVGKRMRLPULLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLPAVYCLDRP 120
DB 61 PLCHTVGKRMRLPULLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLPAVYCLDRP 120
QY 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPATAPVTKI 180
DB 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPATAPVTKI 180
QY 181 CAQCEMESHADGLMEQSSDFVVMRKIKIENGDRKLIQAOKKKKLLKPGPKRKYDT 240
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QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMFS 300
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QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

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RESULT 3
US-10-301-764-6

; Sequence 6, Application US/10301764

; Publication No. US20040039184A1

; GENERAL INFORMATION:

; APPLICANT: Umanaky, Samuil

; TITLE OF INVENTION: A FAMILY OF GENES ENCODING

; APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND

; METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FORSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/301,764

; FILING DATE: 20-No. US20040039184A1-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/937,067

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Lehnhardt, Susan K.

; REGISTRATION NUMBER: 33,943

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 813-5600

; TELEFAX: (650) 494-0792

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-301-764-6

Query Match 100.0%; Score 1730; DB 4; Length 317;

Best Local Similarity 100.0%; Pred. No. 4.6e-169; Indels 0; Gaps 0;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRAAAGGVTAAATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPPQCLDIPADL 60
DB 1 MRAAAGGVTAAATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPPQCLDIPADL 60
QY 61 PLCHTVGKRMRLPULLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLPAVYCLDRP 120
DB 61 PLCHTVGKRMRLPULLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLPAVYCLDRP 120
QY 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPATAPVTKI 180
DB 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPATAPVTKI 180
QY 181 CAQCEMESHADGLMEQSSDFVVMRKIKIENGDRKLIQAOKKKKLLKPGPKRKYDT 240
DB 181 CAQCEMESHADGLMEQSSDFVVMRKIKIENGDRKLIQAOKKKKLLKPGPKRKYDT 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMFS 300
DB 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMFS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

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Db 301 YPCSLYPPFFYGAAEPH 317

RESULT 4
US-10-768-566-1
; Sequence 1, Application US/10768566
; Publication No. US20040259789A1
; GENERAL INFORMATION:
; APPLICANT: Choudhary, K.
; APPLICANT: Choudhary, Roland
; APPLICANT: Ashar, Hena
; APPLICANT: Sayed, Abu
; TITLE OF INVENTION: A METHOD OF TREATING OBESITY AND METABOLIC DISORDERS RELATED TO
; FILE REFERENCE: 69014-B
; CURRENT APPLICATION NUMBER: US/10/768,566
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-10-768-566-1

Query Match 100.0%; Score 1730; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 4, 6e-169; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 0;

Qy 1 MRAAAGAGVTAALALIGALHMAPARCEBYDYGMQAPLHGRSYKPPQCLDIPADL 60
Db 1 MRAAAGAGVTAALALIGALHMAPARCEBYDYGMQAPLHGRSYKPPQCLDIPADL 60
Qy 61 PLCHTVGYRMRLPNLLEHSLAEVYQOASSWPLAKRCHSDTVQVFLCSLFAVCLDRP 120
Db 61 PLCHTVGYRMRLPNLLEHSLAEVYQOASSWPLAKRCHSDTVQVFLCSLFAVCLDRP 120
Qy 121 IYPCRSCEAVRAGCAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPAATPVTKI 180
Db 121 IYPCRSCEAVRAGCAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPAATPVTKI 180
Qy 181 CAQCEMEHSADGLMEQCSSDFVVKMRKEIKIENGDRKLIQAOKKKLKPGLRKQDT 240
Db 181 CAQCEMEHSADGLMEQCSSDFVVKMRKEIKIENGDRKLIQAOKKKLKPGLRKQDT 240
Qy 241 KRLVLMKRGAGCPCPQDLSLGSFLVMGRKVDGQLLMAVYRWDKKMKFAVKEMFS 300
Db 241 KRLVLMKRGAGCPCPQDLSLGSFLVMGRKVDGQLLMAVYRWDKKMKFAVKEMFS 300
Qy 301 YPCSLYPPFFYGAAEPH 317
Db 301 YPCSLYPPFFYGAAEPH 317

RESULT 5
US-10-338-604-5
; Sequence 5, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; FILE REFERENCE: MP101-250P1RM
; CURRENT APPLICATION NUMBER: US/10/338,604
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 314
; TYPE: PRT

; ORGANISM: Mus musculus
US-10-338-604-5

Query Match 93.2%; Score 1613; DB 4; Length 314;
Best Local Similarity 94.9%; Pred. No. 4, 9e-157; Indels 0; Gaps 0;
Matches 295; Conservative 5; Mismatches 11;

Qy 7 AGVTAALALIGALHMAPARCEBYDYGMQAPLHGRSYKPPQCLDIPADLPLCHTV 66
Db 4 AMSARTALALIGALHMAPARCEBYDYGMQAPLHGRSYKPPQCLDIPADLPLCHTV 63
Qy 67 GYKRMRLPNLLEHSLAEVYQOASSWPLAKRCHSDTVQVFLCSLFAVCLDRPIYPCRS 126
Db 64 GYKRMRLPNLLEHSLAEVYQOASSWPLAKRCHSDTVQVFLCSLFAVCLDRPIYPCRS 123
Qy 127 LCEAVRAGCAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPAATPVTKIQAOCCEM 186
Db 124 LCEAVRAGCAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGHLPAATPVTKIQAOCCEM 183
Qy 187 EHSADGLMEQCSSDFVVKMRKEIKIENGDRKLIQAOKKKLKPGLRKQDTKRLVYLH 246
Db 184 EHSADGLMEQCSSDFVVKMRKEIKIENGDRKLIQAOKKKLKPGLRKQDTKRLVYLH 243
Qy 247 MKNAGCPCPQDLSLGSFLVMGRKVDGQLLMAVYRWDKKMKFAVKEMFSYPCSLY 306
Db 244 MKNAGCPCPQDLSLGSFLVMGRKVDGQLLMAVYRWDKKMKFAVKEMFSYPCSLY 303
Qy 307 YPCSLYPPFFYGAAEPH 317
Db 304 YPCSLYPPFFYGAAEPH 314

RESULT 6
US-10-146-474-7
; Sequence 7, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Umehy, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,474
; FILING DATE: 14-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid


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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-146-474-7

Query Match
Best Local Similarity 53.4%; Score 924.5; DB 4; Length 314;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVATATLAL--LGAALHAPARCEBYDYGMQAE--PLH-GRSYSKPPQCLD 55
DB 1 MGIKSGEGRGALGVLLALGALLAVGSASEYDVVSFGSDIGFYQSGRFTKPPQCLD 60
QY 56 IPADPLCHTGVYKRRRLNNLLEHESLAVYKQOASSWPLLAKRGHSDTQVFLCSIFAVY 115
DB 61 IPADRLCHNVGYKKKVLNNLLEHETMAVYKQOASSWPLLNKNCHAGQVFLCSIFAVY 120
QY 116 CUDRPIYPCRSICEAVRAGCAPLMEAYGFPWPEMLHCHKEPLDNDCLAVQGH--LPATA 174
DB 121 CUDRPIYPCRMICEAVRDSCEPVMQPFQGYWPEMLKCDKFP--BGDVCIAMTPPNATEASK 179
QY 175 PVTYKICAOCEMHSADGLMEQSSDFVVMKRIKEIKIENGDRKLIGAOKKKLXKGP 234
DB 180 PGCTVCPCCDNEKSEALIEHLCSSEFALRMKIKKVKKENGDKKIV--PKKKKPLKGP 237
QY 235 LKAKDTKRLVLMKNGACGCPQOLDLAGSFLVMGRKYDQGLLMAVYRMDKKNEMKFA 294
DB 238 IKKKDLKTLVLYLKNAGDCPCHQLDNLSHHFLIMGRKXVSQYLLTAHKMDKKNKFEKNF 297
QY 295 VKMFSPYCSLYYPPF 310
DB 298 MKMKMKNHECPTQSVF 313

RESULT 7
US-10-138-434A-3
Sequence 3, Application US/10138434A
Publication No. US20030175864A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: Rubin, Jeffrey S.
APPLICANT: Finch, Paul
APPLICANT: Aaronson, Stuart
APPLICANT: He, Xi
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN FRP AND FRAGMENTS THEREOF
FILE REFERENCE: 4239-62520
CURRENT APPLICATION NUMBER: US/10/138,434A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 09/087,031
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: US 60/050,495
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: US 60/050,417
PRIOR FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-138-434A-3

Query Match
Best Local Similarity 53.4%; Score 924.5; DB 4; Length 314;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVATATLAL--LGAALHAPARCEBYDYGMQAE--PLH-GRSYSKPPQCLD 55
DB 1 MGIKSGEGRGALGVLLALGALLAVGSASEYDVVSFGSDIGFYQSGRFTKPPQCLD 60
QY 56 IPADPLCHTGVYKRRRLNNLLEHESLAVYKQOASSWPLLAKRGHSDTQVFLCSIFAVY 115
DB 61 IPADRLCHNVGYKKKVLNNLLEHETMAVYKQOASSWPLLNKNCHAGQVFLCSIFAVY 120
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DB 61 IPADRLCHNVGYKKKVLNNLLEHETMAVYKQOASSWPLLNKNCHAGTQVFLCSIFAVY 120
QY 116 CUDRPIYPCRSICEAVRAGCAPLMEAYGFPWPEMLHCHKEPLDNDCLAVQGH--LPATA 174
DB 121 CUDRPIYPCRMICEAVRDSCEPVMQPFQGYWPEMLKCDKFP--BGDVCIAMTPPNATEASK 179
QY 175 PVTYKICAOCEMHSADGLMEQSSDFVVMKRIKEIKIENGDRKLIGAOKKKLXKGP 234
DB 180 PGCTVCPCCDNEKSEALIEHLCSSEFALRMKIKKVKKENGDKKIV--PKKKKPLKGP 237
QY 235 LKAKDTKRLVLMKNGACGCPQOLDLAGSFLVMGRKYDQGLLMAVYRMDKKNEMKFA 294
DB 238 IKKKDLKTLVLYLKNAGDCPCHQLDNLSHHFLIMGRKXVSQYLLTAHKMDKKNKFEKNF 297
QY 295 VKMFSPYCSLYYPPF 310
DB 298 MKMKMKNHECPTQSVF 313
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RESULT 8
US-10-301-764-7
Sequence 7, Application US/10301764
Publication No. US20040039184A1
GENERAL INFORMATION:
APPLICANT: Umaneky, Samuel
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-NOV-02
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPES: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-301-764-7

Query Match
Best Local Similarity 53.4%; Score 924.5; DB 4; Length 314;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVATATLAL--LGAALHAPARCEBYDYGMQAE--PLH-GRSYSKPPQCLD 55
DB 1 MGIKSGEGRGALGVLLALGALLAVGSASEYDVVSFGSDIGFYQSGRFTKPPQCLD 60
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QY 56 IPADLPCHTVGKRMRLPNLLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAV 115
DB 61 IPADLPCHTVGKRMRLPNLLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAV 120
QY 116 CIDRPIYPCRSICEAVRAGCAPLMEAYGFPWPMHLCHKFPLDNDLCIAVQFGH-LPATA 174
DB 121 CIDRPIYPCRSICEAVRAGCAPLMEAYGFPWPMHLCHKFPLDNDLCIAVQFGH-LPATA 179
QY 175 PRPTKICACCEMESHADGLMEQCSSDFVVMKRIKIKIENGDRKLIQAOKKKKLLKPGP 234
DB 180 PGSTVCPDNLKSEALIEHLCASEFALRMKIKIENGDRKLIQAOKKKKLLKPGP 237
QY 235 LKRDITKRLVLYLHKNAGACPCPOLDSLASSFLVMGRKVDGOLLMAVYRMDKKNKEMKFA 294
DB 238 IKKDKLKLVLVLYLHKNAGACPCPOLDSLASSFLVMGRKVDGOLLMAVYRMDKKNKEMKFA 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKMKHNECPTFQSVF 313

RESULT 9

US-10-666-851-2
; Sequence 2, Application US/10666851
; Publication No. US20040115195A1
; GENERAL INFORMATION:
; APPLICANT: Bodine, Peter
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING SECRETED FRIZZLED
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 00630/100M91-US1
; CURRENT APPLICATION NUMBER: US/10/666,851
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 10/169,545
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/412,379
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-666-851-2

Query Match 53.4%; Score 924.5; DB 4; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.5e-86;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGGVRTAALAL--IGALHMAPARCEEDYDYGMOA--PLH-GRSYSKPPQCD 55
DB 1 MGISSBEGGRKAGLAVLALGALALAVGSASBYDVSFQSDIGYQSGRFTTKPQCDV 60
QY 56 IPADLPCHTVGKRMRLPNLLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAV 115
DB 61 IPADLPCHTVGKRMRLPNLLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAV 120
QY 116 CIDRPIYPCRSICEAVRAGCAPLMEAYGFPWPMHLCHKFPLDNDLCIAVQFGH-LPATA 174
DB 121 CIDRPIYPCRSICEAVRAGCAPLMEAYGFPWPMHLCHKFPLDNDLCIAVQFGH-LPATA 179
QY 175 PRPTKICACCEMESHADGLMEQCSSDFVVMKRIKIKIENGDRKLIQAOKKKKLLKPGP 234
DB 180 PGSTVCPDNLKSEALIEHLCASEFALRMKIKIENGDRKLIQAOKKKKLLKPGP 237
QY 235 LKRDITKRLVLYLHKNAGACPCPOLDSLASSFLVMGRKVDGOLLMAVYRMDKKNKEMKFA 294
DB 238 IKKDKLKLVLVLYLHKNAGACPCPOLDSLASSFLVMGRKVDGOLLMAVYRMDKKNKEMKFA 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKMKHNECPTFQSVF 313

RESULT 10
US-10-788-792-148
; Sequence 148, Application US/10788792
; Publication No. US20040191819A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
; LENGTH: 314
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-788-792-148

Query Match 53.4%; Score 924.5; DB 4; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.5e-86;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGGVRTAALAL--IGALHMAPARCEEDYDYGMOA--PLH-GRSYSKPPQCD 55
DB 1 MGISSBEGGRKAGLAVLALGALALAVGSASBYDVSFQSDIGYQSGRFTTKPQCDV 60
QY 56 IPADLPCHTVGKRMRLPNLLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAV 115
DB 61 IPADLPCHTVGKRMRLPNLLEHESLAEVYKQASWMLPLAKRCHSDTQVFLCSLFAV 120
QY 116 CIDRPIYPCRSICEAVRAGCAPLMEAYGFPWPMHLCHKFPLDNDLCIAVQFGH-LPATA 174
DB 121 CIDRPIYPCRSICEAVRAGCAPLMEAYGFPWPMHLCHKFPLDNDLCIAVQFGH-LPATA 179
QY 175 PRPTKICACCEMESHADGLMEQCSSDFVVMKRIKIKIENGDRKLIQAOKKKKLLKPGP 234
DB 180 PGSTVCPDNLKSEALIEHLCASEFALRMKIKIENGDRKLIQAOKKKKLLKPGP 237
QY 235 LKRDITKRLVLYLHKNAGACPCPOLDSLASSFLVMGRKVDGOLLMAVYRMDKKNKEMKFA 294
DB 238 IKKDKLKLVLVLYLHKNAGACPCPOLDSLASSFLVMGRKVDGOLLMAVYRMDKKNKEMKFA 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKMKHNECPTFQSVF 313

RESULT 11
US-10-756-149-5611
; Sequence 5611, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nabeela
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5611
; LENGTH: 314
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-756-149-5611

Query Match 53.4%; Score 924.5; DB 5; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.5e-86;

LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-10-425-586-4

Query Match 53.0%; Score 917; DB 4; Length 338;
Best Local Similarity 57.9%; Pred. No. 2.3e-85;
Matches 179; Conservative 50; Mismatches 70; Indels 10; Gaps 7;

QY 8 GGVRTAALLLLGALHMAPAR--CEBYDYGGQAE--PLH-GRSYKPPQCLDIPADLPL 62
DB 8 GGRRGALGLVL-ALGGASGRGIGSEYDYVSFQSDIGPYQSGRFYTKPPQCVDIPADLPL 66
QY 63 CHTVGYKRMRLPNLLEHESLAEVKQOASSWMLPLAKRCHSDTQVFLCSLFAVCLDRPIY 122
DB 67 CHNVGKIKKRVLPNLLEHETMAEVKQOASSWVPLANKKCHAGTQVFLCSLFAVCLDRPIY 126
QY 123 PCRSLCEAVRAGCAPLMEAYGFPWPBMLCHKFPLDNDLCIAVQFGH-LPATAAPVTYKIC 181
DB 127 PCRMLCEAVRDSCEPVMQFPGFYWPBMLKCDKFP--EGDVCIAMTPPNATEASKPGQTTVC 185
QY 182 AOCSEMSADGLMEQCSSDFVYVKRIKIKIENGDRKLIGAOKKKLLKPGPLKRDYK 241
DB 186 PCQDNEKSEAIIEHLCASEFALRMKIKKVENGDKKIV--PKKKKPLKLGPIKKKDLK 243
QY 242 RLVIHMKNGAGCPQPDLSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMFSY 301
DB 244 KLVLYLKNKGADCPCHQDNLSHHFLIMGRKVKYSQYLLTAHKMDKKNKEFKNFMKMKKNH 303
QY 302 PCSLYYPPF 310
DB 304 ECPTFQSVF 312

RESULT 15
US-10-466-136-4
Sequence 4, Application US/10466136
Publication No. US20040077828A1
GENERAL INFORMATION:
APPLICANT: Rudin, Jeffery et al.,
TITLE OF INVENTION: SFRP AND PEPTIDE MOTIFS THAT INTERACT WITH SFRP AND
FILE REFERENCE: 4239-61994
CURRENT APPLICATION NUMBER: US/10/466,136
PRIOR FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: US 60/260,908
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 338
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-466-136-4

Query Match 53.0%; Score 917; DB 4; Length 338;
Best Local Similarity 57.9%; Pred. No. 2.3e-85;
Matches 179; Conservative 50; Mismatches 70; Indels 10; Gaps 7;

QY 8 GGVRTAALLLLGALHMAPAR--CEBYDYGGQAE--PLH-GRSYKPPQCLDIPADLPL 62
DB 8 GGRRGALGLVL-ALGGASGRGIGSEYDYVSFQSDIGPYQSGRFYTKPPQCVDIPADLPL 66
QY 63 CHTVGYKRMRLPNLLEHESLAEVKQOASSWMLPLAKRCHSDTQVFLCSLFAVCLDRPIY 122
DB 67 CHNVGKIKKRVLPNLLEHETMAEVKQOASSWVPLANKKCHAGTQVFLCSLFAVCLDRPIY 126
QY 123 PCRSLCEAVRAGCAPLMEAYGFPWPBMLCHKFPLDNDLCIAVQFGH-LPATAAPVTYKIC 181
DB 127 PCRMLCEAVRDSCEPVMQFPGFYWPBMLKCDKFP--EGDVCIAMTPPNATEASKPGQTTVC 185

QY 182 AOCSEMSADGLMEQCSSDFVYVKRIKIKIENGDRKLIGAOKKKLLKPGPLKRDYK 241
DB 186 PCQDNEKSEAIIEHLCASEFALRMKIKKVENGDKKIV--PKKKKPLKLGPIKKKDLK 243
QY 242 RLVIHMKNGAGCPQPDLSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMFSY 301
DB 244 KLVLYLKNKGADCPCHQDNLSHHFLIMGRKVKYSQYLLTAHKMDKKNKEFKNFMKMKKNH 303
QY 302 PCSLYYPPF 310
DB 304 ECPTFQSVF 312

Search completed: March 22, 2006, 22:46:46
Job time : 166 secs

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CC AAW37814), human hSARF1 (see AAW37816) and hSARF2 (see AAW37817) proteins
CC are also claimed. hSARF3 is expressed predominantly in pancreas. SARF
CC polypeptides can be obtained from recombinant host cells. Antibodies
CC specific for SARF polypeptides can be used in immunoassays for detecting
CC levels of expression of SARF, particularly for diagnosis or monitoring of
CC diseases associated with SARF expression. Specifically, they are used to
CC detect cancer of the prostate or breast (by detecting hSARF1 and 2,
CC respectively). SARF polypeptides and nucleic acids can also be used to
CC treat these cancers, or more generally apoptosis-related disease (e.g.
CC infection with HIV or reperfusion injury), also (not claimed) to prevent
CC apoptosis in cultured cells, to improve preservation of organs for
CC transplantation, for in situ preservation for by-pass operations and to
CC treat dermatological disorders. SARF polypeptides can also be used to
CC identify agents, potentially useful therapeutically, that modulate the
CC effects of SARF on mit-1/frizzled protein interaction

XX
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 1730; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-176;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGGVRTRALALLGALHMAPARCEVDYVGMAEPHGRSYKPPQCLDIPDL 60
DB 1 MRAAAGGVRTRALALLGALHMAPARCEVDYVGMAEPHGRSYKPPQCLDIPDL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
QY 121 IYPCSLCEAVAVAGACAPLMEAVGFPMPEMLHCHKFPLDNDLCIAVOFGHLPTAPPVTKI 180
DB 121 IYPCSLCEAVAVAGACAPLMEAVGFPMPEMLHCHKFPLDNDLCIAVOFGHLPTAPPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDPFVVKRIKEIKIENDRKLIGAOKKKLLKGPPLKPKRT 240
DB 181 CAQCEMESHADGLMEQCSSDPFVVKRIKEIKIENDRKLIGAOKKKLLKGPPLKPKRT 240
QY 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLLMAVYRMDKKNKEMKFAVKFMS 300
DB 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLLMAVYRMDKKNKEMKFAVKFMS 300
QY 301 YPCSLYYPFFYGABPH 317
DB 301 YPCSLYYPFFYGABPH 317

RESULT 2
ADA38289
ID ADA38289 standard; protein; 317 AA.
AC ADA38289;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX
DE Human secreted apoptosis related protein (SARF) 3.
XX
XX
KW Human; metabolic disorder; Secreted Apoptosis-Related Proteins 3; SARF3;
KW obesity; overweight; diabetes; insulin resistance; cachexia; anorexia;
KW beta-catenin; leptin; insulin sensitivity; food intake;
KW body weight change; glucose tolerance; hyperplastic growth;
KW cell differentiation; programmed cell death; apoptosis;
KW hypertrophic growth; modulator; agonist; antagonist; antisense; ribozyme;
KW lipid; glucose; insulin; adipocyte; differentiation; adipose cell;
KW adipocyte; anorectic; antidiabetic; immunomodulator.

OS Homo sapiens.
XX
XX
PN US2003143610-A1.
XX
XX
PD 31-JUL-2003.
XX
XX
PF 08-JAN-2003; 2003US-00338604.

XX
XX
PR 08-JAN-2003; 2003US-0346523P.
XX
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX
PI Xu H;
XX
XX
DR WPI; 2003-635956/60.
DR N-PADB; ADA38288, ADA38290.
XX
XX
PT Identifying a compound for treating a metabolic disorder, e.g., diabetes-
PT Related Proteins 3 (SARF3) nucleic acid expression or polypeptide
XX activity.
XX
PS Claim 6; SEQ ID NO 2; 35bp; English.
XX
XX
CC The invention discloses a method for identifying a compound for treating
CC a metabolic disorder which comprises assaying the ability of the compound
CC to modulate Secreted Apoptosis-Related Proteins 3 (SARF3) nucleic acid
CC expression or polypeptide activity. Also claimed are methods for
CC modulating SARF3 mediated metabolic activity, treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity and a pharmaceutical formulation for
CC treating metabolic disorders. The metabolic disorders comprise obesity,
CC overweight, diabetes, insulin resistance, cachexia or anorexia. The
CC ability of the compound to modulate SARF3 nucleic acid expression or
CC polypeptide activity is determined by detecting a SARF3 activity of a
CC cell, or by detecting modulation of the level of beta-catenin, leptin or
CC insulin sensitivity, food intake, body weight change, glucose tolerance,
CC hyperplastic growth, cell differentiation, programmed cell death or
CC hypertrophic growth. Modulating SARF3 mediated metabolic activity
CC comprises contacting a cell or tissue expressing the SARF3 with a SARF3
CC modulator. The compound or modulator comprises a small molecule SARF3
CC agonist or antagonist or inverse agonist, anti-SARF3 antibody, antisense
CC SARF3 molecule or ribozyme. The SARF3 mediated metabolic activity
CC comprises the ability to modulate lipid, glucose or insulin metabolism,
CC adipocyte growth, the differentiation of adipose cell progenitors into
CC adipocytes or programmed cell death. Treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity comprises administering a SARF3
CC modulator. The compound is an oligonucleotide encoding an antisense or
CC ribozyme molecule that targets SARF3 transcripts and inhibits translation
CC or an oligonucleotide that forms a triple helix with the promoter of the
CC SARF3 gene and inhibits transcription. The sequence presented is the
CC human SARF3 protein.
XX
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 1730; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-176;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGGVRTRALALLGALHMAPARCEVDYVGMAEPHGRSYKPPQCLDIPDL 60
DB 1 MRAAAGGVRTRALALLGALHMAPARCEVDYVGMAEPHGRSYKPPQCLDIPDL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
QY 121 IYPCSLCEAVAVAGACAPLMEAVGFPMPEMLHCHKFPLDNDLCIAVOFGHLPTAPPVTKI 180
DB 121 IYPCSLCEAVAVAGACAPLMEAVGFPMPEMLHCHKFPLDNDLCIAVOFGHLPTAPPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDPFVVKRIKEIKIENDRKLIGAOKKKLLKGPPLKPKRT 240
DB 181 CAQCEMESHADGLMEQCSSDPFVVKRIKEIKIENDRKLIGAOKKKLLKGPPLKPKRT 240
QY 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLLMAVYRMDKKNKEMKFAVKFMS 300
DB 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLLMAVYRMDKKNKEMKFAVKFMS 300

QY	301	YPCSLYYPFFYGAE	PH	317
Db	301	YPCSLYYPFFYGAE	PH	317

RESULT 3
ADM67242
ID ADM67242 standard; protein; 317 AA

AC	ADM67242;
XX	
DT	03-JUN-2004 (first entry)

DE Human homologue of murine adipocyte specific SFRP-5 protein SeqID 604.

KM human; adipocyte specific; adipose tissue; anti-obesity;
KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes
KM adipogenesis; hypertension; cardiovascular disease; anorectic;
KM antidiabetic; hypotensive; sFRP-5.

OS Homo sapiens.

PN WO2004011618-A2

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMGE-) HMGENE INC

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66969.

PT Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets. By differential gene expression analysis between adipose tissue or stromal vascular tissue of mice of different genotypes.

PS Disclosure; SEQ ID NO 604; 91pp; English.

This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anti-obesity pharmaceutical compositions. Specifically, it refers to a high mobility group I-C protein (HMGI-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or serosal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C ^{-/-}, ob/ob, or HMGI-C ^{-/-} ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and hypotensive activities. This polypeptide sequence is a human homologue of a murine adipocyte specific protein sequence of the invention.

SQ Sequence 317 AA;

Query Match	100.0%	Score 1730;	DB 8;	Length 317;
Best Local Similarity	100.0%;	Pred. No. 2.5e-176;		
Matches 317; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

Qy 1 MRAAAGGVRTAATALLGALHPARCEEYDYGWQAEPLHGRSYSKPPCLDIPADL 6C

Db 1 MRAAAGGVRTAATALLGALHPARCEEYDYGWQAEPLHGRSYSKPPCLDIPADL 6C

Qy	Db
61 PLCHTVGYKRMRLPNLLIEHESLAETKQASSWLPPLAKRCHSDTQVFLCSLPAPVCLDRP	61 PLCHTVGYKRMRLPNLLIEHESLAETKQASSWLPPLAKRCHSDTQVFLCSLPAPVCLDRP

121 IYPCRSICEAVRAGCAPLMEAYGFPWPPEMLHCHKFPDNDLCIAVQFGHLPATAPVTKI 180

Db 121 IYPCRSICEAVRAGCAPLMEAYGFPPWPEMLCHKFPLDNDLCIAVQEGHLPATAPVTKI 180

QY 181 CAQCEMEHSADGLMEQMCSSDFVVKRIKEIKIENGDRKLTGAQKKKLLKPGPLKRDY 240

Db 181 CAQCEMEHSADGLMEQMCSSDFVVKRIKEIKIENGDRKLI GAQKKKLLKGPLK R KDT 240

RESULT 4
ADP56062
ID ADP56062 standard; protein; 317 AA

AC ADP56062;

DT 18-NOV-2004 (first entry)

DE Human PRO protein sequence SEQ ID NO:2038.

human; PBO; immune related disease; inflammatory immune response;
immune response stimulation; antiallergic; antianaemic; antiarthritis;
antidiabetic; antidiabetic; antiinflammatory; antipsoriasis;
antirheumatic; antitumor; CNS; dermatological; gastrointestinal;
immunologic; immunostimulant; immunosuppressive; muscular
neurotrophic; neuroprotective; osteoporotic; respiratory; vasotropic;
viral; gene therapy.

OS Homo sapiens.

PN WO2004039956-A2.

PD 13-MAY-2004

PF 28-OCT-2003; 2003WO-US034381.

PR 29-OCT-2002; 2002US-0422472P

PA (GETH) GENENTECH INC.

PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

XX

DR N-PSDB; ADP56061.

PT New PRO polynucle

PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematous, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.

PS Claim 1; SEQ ID NO 2038; 3009pp; English

CC The present invention describes an isolated pro-nucleic acid (1). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a pro-peptides; (4) an
CC isolated pro polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the

CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have anti-allergic, anti-inflammatory, anti-arthritic,
CC antidiabetic, antidiabetic, anti-inflammatory, antiparasitic,
CC antirheumatic, anticholesteric, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC neoplastic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.

CC Sequence 317 AA;

Query Match 100.0%; Score 1730; DB 8; Length 317;
Best Local Similarity 100.0%; Pred. No. 2,5e-176;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGAGVTRTALALLGALHMAPARCEVDYGMQAEPLHGRSYSKPQCLDIPADL 60
DB 1 MRAAAGAGVTRTALALLGALHMAPARCEVDYGMQAEPLHGRSYSKPQCLDIPADL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTQVFLCSLFAVCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTQVFLCSLFAVCLDRP 120
QY 121 IYPCRSLSCEAVRAGACAPLMEAYGFPWPBMLHCHKRPDLNDLCIAVOFGHLPATAPVTXI 180
DB 121 IYPCRSLSCEAVRAGACAPLMEAYGFPWPBMLHCHKRPDLNDLCIAVOFGHLPATAPVTXI 180
QY 181 CAQCEMEHSADGLMEQWSSDFVVKRIKEIKIENGDRKLGAOKKKLKPGLKRDY 240
DB 181 CAQCEMEHSADGLMEQWSSDFVVKRIKEIKIENGDRKLGAOKKKLKPGLKRDY 240
QY 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKEMFS 300
DB 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKEMFS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

RESULT 5

ID AAW73507 standard; protein; 317 AA.

AAW73507;

01-MAR-1999 (first entry)

Human ATG-1709 protein.

Human; ATG-1709 protein; secreted ligand; 7-Transmembrane receptor;
heart disease; hypertension; cardiovascular disease; kidney disease;
obesity; insulin resistance; diabetes; Central Nervous System disorder;
therapy; sRRP-1.

Homo sapiens.

EP879885-A1.

25-NOV-1998.

16-JAN-1999; 98BP-00300313.

XX 23-MAY-1997; 97US-0047691P.
PR 08-AUG-1997; 97US-00907808.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
XX
PI Hu B, Zhu Y;
XX WPI; 1998-596877/51.
DR N-PSDB; AAW08946.
XX
PT New human secreted protein ATG-1709 polypeptide and polynucleotide -
PT useful as diagnostic reagents and for diagnosing, prevention and
PT treatment of Central Nervous System diseases and diabetes.

Claim 11; Page 6; 28pp; English.

CC This sequence represents the human ATG-1709 protein of the invention. ATG
CC -1709 is related to human secreted ligands for 7-Transmembrane receptors
CC and similar to murine sRRP-1. ATG-1709 polypeptides and polynucleotides
CC are useful for diagnosing susceptibility to diseases by detecting
CC mutations in the ATG-1709 gene using probes containing the ATG-1709
CC nucleotide sequence, and can diagnose diseases associated with ATG-1709
CC imbalance by determining ATG-1709 polypeptide expression levels. ATG-1709
CC polypeptides can be used to screen for agonists and antagonists which
CC bind the ATG-1709 polypeptide. These can be used in treatment to activate
CC or inhibit ATG-1709 activity, in addition to direct administration of
CC antisense sequences to prevent expression, or ATG-1709 polypeptides to
CC treat conditions associated with a lack of ATG-1709. Gene therapy may
CC also be used to affect endogenous ATG-1709 expression. ATG-1709
CC antibodies are useful for inducing an immune response to immune and
CC prevent diseases, and for isolating ATG-1709 clones or purifying the
CC polypeptides by affinity chromatography. ATG-1709 polypeptides can be
CC administered directly or as a vaccine to inoculate against disease.
CC diseases diagnosed, prevented or treated include: heart disease;
CC hypertension; cardiovascular diseases; kidney diseases; obesity; insulin
CC resistance; diabetes and Central Nervous System (CNS) diseases. The ATG-
CC 1709 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis

Sequence 317 AA;

Query Match 99.6%; Score 1723; DB 2; Length 317;
Best Local Similarity 99.7%; Pred. No. 1.4e-175;
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAAAGAGVTRTALALLGALHMAPARCEVDYGMQAEPLHGRSYSKPQCLDIPADL 60
DB 1 MRAAAGAGVTRTALALLGALHMAPARCEVDYGMQAEPLHGRSYSKPQCLDIPADL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTQVFLCSLFAVCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTQVFLCSLFAVCLDRP 120
QY 121 IYPCRSLSCEAVRAGACAPLMEAYGFPWPBMLHCHKRPDLNDLCIAVOFGHLPATAPVTXI 180
DB 121 IYPCRSLSCEAVRAGACAPLMEAYGFPWPBMLHCHKRPDLNDLCIAVOFGHLPATAPVTXI 180
QY 181 CAQCEMEHSADGLMEQWSSDFVVKRIKEIKIENGDRKLGAOKKKLKPGLKRDY 240
DB 181 CAQCEMEHSADGLMEQWSSDFVVKRIKEIKIENGDRKLGAOKKKLKPGLKRDY 240
QY 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKEMFS 300
DB 241 KRLVLMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKEMFS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

RESULT 6
ADA38292

ID ADA38292 standard; protein; 314 AA.
XX
AC ADA38292;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse secreted apoptosis related protein (SARP) 3.
XX
KW Mouse; metabolic disorder; Secreted Apoptosis-Related Proteins 3; SARP3;
KW obesity; overweight; diabetes; insulin resistance; cachexia; anorexia;
KW beta-catenin; leptin; insulin sensitivity; food intake;
KW body weight change; glucose tolerance; hyperplastic growth;
KW cell differentiation; programmed cell death; apoptosis;
KW hypertrophic growth; modulator; agonist; antagonist; antisense; ribozyme;
KW lipid; glucose; insulin; adipocyte; differentiation; adipose cell;
KW adipocyte; anorectic; antidiabetic; immunomodulator.
XX
OS Mus musculus.
XX
PN US2003143610-A1.
XX
PD 31-JUL-2003.
XX
PF 08-JAN-2003; 2003US-00338604.
XX
PR 08-JAN-2002; 2002US-0346523P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Xu H;
XX
DR WPI; 2003-635956/60.
DR N-PSDB; ADA38291, ADA38293.
XX
PT Identifying a compound for treating a metabolic disorder, e.g., diabetes
PT by assaying the ability of the compound to modulate a Secreted Apoptosis-
PT Related Proteins 3 (SARP3) nucleic acid expression or polypeptide
PT activity.
XX
PS Claim 6; SEQ ID NO 5; 35pp; English.
XX
XX The invention discloses a method for identifying a compound for treating
XX a metabolic disorder which comprises assaying the ability of the compound
XX to modulate Secreted Apoptosis-Related Proteins 3 (SARP3) nucleic acid
XX expression or polypeptide activity. Also claimed are methods for
XX modulating SARP3 mediated metabolic activity, treating a subject having a
XX metabolic disorder characterised by aberrant SARP3 nucleic acid
XX expression or polypeptide activity and a pharmaceutical formulation for
XX treating metabolic disorders. The metabolic disorders comprise obesity,
XX overweight, diabetes, insulin resistance, cachexia or anorexia. The
XX ability of the compound to modulate SARP3 nucleic acid expression or
XX polypeptide activity is determined by detecting a SARP3 activity of a
XX cell, or by detecting modulation of the level of beta-catenin, leptin or
XX insulin sensitivity, food intake, body weight change, glucose tolerance,
XX hyperplastic growth, cell differentiation, programmed cell death or
XX hypertrophic growth. Modulating SARP3 mediated metabolic activity
XX comprises contacting a cell or tissue expressing the SARP3 with a SARP3
XX modulator. The compound or modulator comprises a small molecule SARP3
XX agonist or antagonist or inverse agonist, anti-SARP3 antibody, antisense
XX SARP3 molecule or ribozyme. The SARP3 mediated metabolic activity
XX comprises the ability to modulate lipid, glucose or insulin metabolism,
XX adipocyte growth, the differentiation of adipose cell progenitors into
XX adipocytes or programmed cell death. Treating a subject having a
XX metabolic disorder characterised by aberrant SARP3 nucleic acid
XX expression or polypeptide activity comprises administering a SARP3
XX modulator. The compound is an oligonucleotide encoding an antisense or
XX ribozyme molecule that targets SARP3 transcripts and inhibits translation
XX or an oligonucleotide that forms a triple helix with the promoter of the
XX SARP3 gene and inhibits transcription. The sequence presented is the
XX mouse SARP3 protein.
XX
XX Sequence 314 AA;

Query Match 93.2%; Score 1613; DB 6; Length 314;
Best Local Similarity 94.9%; Pred. No. 8,66-164;
Matches 295; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 7 AGCVRTAALALILGLHMAPARCEEDYDYGQAEPLHGRSRSKPPQCLDIPADLPLCHTV 66
DB 4 AMSARTALALILGLHGAPTRGQEDYDYGQAEPLHGRSRSKPPQCLDIPADLPLCHTV 63
QY 67 GKRRRLPMLHESLAIEVQOASMLPLAKRCHSDQVFLCSLFAVYCLDRPIYPCRS 126
DB 64 GKRRRLPMLHESLAIEVQOASMLPLAKRCHSDQVFLCSLFAVYCLDRPIYPCRS 123
QY 127 ICEAVRAGCAPLMEAYGFPWPEMLCHKPPLDNDLCIAVQFGLPATAPVTKICAQCEM 186
DB 124 ICEARAGCAPLMEAYGFPWPEMLCHKPPLDNDLCIAVQFGLPATAPVTKICAQCEM 183
QY 187 EHSADGLMEOWCSSPFFVYKMKIKETKINGDRKLIQAOKKKLLKPGPLKRDYRLVH 246
DB 184 EHSADGLMEOWCSSPFFVYKMKIKETKINGDRKLIQAOKKKLLKAGPLKRDYRLVH 243
QY 247 MKNAGACPCPODLSLAGSFLVMGRKYDQQLLMAYVRMDKXKEMKFAVKFMFSYPCSLY 306
DB 244 MKNAGACPCPODNDITGSEFLVMGRKYDQQLLMAYVRMDKXKEMKFAVKFMFSYPCSLY 303
QY 307 YPFFYGAAEPH 317
DB 304 YPFFYGAAEPH 314

RESULT 7
ID ADM67241
XX ADM67241 standard; protein; 314 AA.
XX
AC ADM67241;
XX
DT 03-JUN-2004 (first entry)
XX
DE Murine adipocyte specific sFRP-5 protein SegID 603.
XX
KW murine; mouse; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; sFRP-5.
XX
OS Mus musculus.
XX
PN W02004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US0233684.
XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGE-) HMGENE INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR WPI; 2004-143846/14.
DR N-PSDB; ADM69368.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Claim 47; SEQ ID NO 603; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
XX over-expressed in adipose tissue and as such it provides targets for anti-
XX obesity pharmaceutical compositions. Specifically, it refers to a high
XX mobility group I-C protein (HMGI-C) that is associated with obesity and

XX		Human Frizzled-related protein (FRP).
KX	FRP; frizzled-related protein; human; Wnt binding domain; recombinant;	
KW	Cytokine; cell growth; differentiation; migration; tumour suppressor;	
KV	Oncogenesis; cancer; Drosophila; Wingless protein; Wnt; neoplasia;	
XX	transgenic; therapeutic.	
OS	Homo sapiens.	
KX		
FH	Key Location/Qualifiers	
FT	Peptide 1..28	
FT	/note= "putative signal sequence"	
FT	Misc-difference 14 /note= "encoded by a CAG insertion sequence observed in some cDNA constructs"	
FT	Protein 29..314	
FT	/note= "mature protein"	
FT	Domain 57..166	
FT	/note= "Wnt binding domain"	
FT	Modified-site 173..175	
FT	/note= "Asn is potentially N-glycosylated"	
FT	Modified-site 263..265	
FT	/note= "Asn is potentially N-glycosylated"	
PN	MO9654325-AI.	
PD	03-DEC-1998.	
XX		
PF	29-MAY-1998; 98WO-US010974.	
PR	29-MAY-1997; 97US-0050417P.	
XX		
PA	23-JUN-1997; 97US-0050495P.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Rubin JS, Finch P, Aaronson S, He X;	
DR	WI; 1999-059840/05.	
N-PSDB; AAVB84395.		
XX		
PT	New human frizzled-related protein and associated nucleic acid, probes,	
PT	vectors - transformants, antibodies and transgenic animals, used to	
PT	inhibit signalling by Wnt-family cytokines, potentially useful as tumour	
PT	suppressors.	
XX		
PS	Claim 5, Fig 1C; 83pp; English.	
XX		
CC	This represents a human FRP (frizzled-related protein) polypeptide. The	
CC	FRP polypeptide comprises a wnt binding domain. Host cells containing a	
CC	vector comprising the FRP nucleic acid are used to produce recombinant	
CC	FRP which is a secreted antagonist of Wnt-family cytokines. FRP is	
CC	involved in cell growth, differentiation and migration and possibly can	
CC	act as tumour suppressor. FRP is used in studies on oncogenesis and in	
CC	design of cancer treatments, e.g. administration of cells transfected	
CC	with the FRP gene. Antibodies that bind specifically to FRP are used to	
CC	detect FRP in immunoassays. FRP can also be used to detect specific	
CC	binding proteins (specifically the Drosophila Wingless protein, but more	
CC	generally any Wnt molecule) in a sample, particularly for monitoring	
CC	progress of neoplasia. Transgenic animals in which somatic and germ cells	
CC	contain a transgene from human FRP are used to develop and screen	
CC	therapeutic agents	
SQ	Sequence 314 AA;	
Query Match	53.4%; Score 924.5; DB 2; Length 314;	
Best Local Similarity	56.6%; Pred. No. 5,9e+90;	
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6		
Ddb	1 MRANAACGGTAAATL--LGALHWAPRCCEVDYQGAE--PLH-GRSYKPPQCID 55 1 MOIGSGEGGRRAALGCVLLAAGALLAVGSABFDVSFGSDIQPGQSRRFTRKPQCVD 60 56 IPADIPLCHTVGYKKWRRLPNILLESFLAEVKOASSWPFLAKRCHSDTOVFCLSAFAV 115	

Dd		61	IPADLALCNVGYKKKAVLPNLLHEHTMAEYVQASWSVPPLKNKGCHAGTQVPLCSLFAPV	120
Oy		116	CLDRPIYPGRLCEAARACAPLMFAAYPRPPEMLHCKEPPLDNDLCIAVOFGH-LPATA	174
Dd		121	CLDRPIYPGRLCEAARVDSCPEVMQPFQFVPEMLCKDKFP-EGDVCIAMTPPNATEASK	179
Oy		175	PPTATKCAOCENEHSHADSLMEQMSCSDPVGMKRKEIKETENGDPKLIGAKKKRLLKRP	234
Dd		180	PGCTTCPCPDNELSEALIEHLCASEPALNRKLIKVEVKRGDKKI--PKKKKPCLKGP	237
Oy		235	LKRDTRKRLVLHMKNAGACGPCPOLDSLAFSGFLVMGRKVDQLLMAYVRMDKNGEMKFA	294
Dd		238	IKKKDLKGLVLYLNKGADCPCHQJLDNLSHFLINGRKKSQYLTLAIHKDDKNNKEKNF	297
Oy		295	VKEFMSPYPCSLYYPPF	310
Dd		298	MKGKGNHECPTFSQSVF	313
RESULT 10				
ID	ABP72785			
XX	ABP72785	standard; protein; 314 AA.		
AC	ABP72785;			
DT	17-JUN-2003	(first entry)		
XX				
DE		Human secreted frizzled related protein.		
KM		Human, secreted frizzled related protein; sFRP, ischemia; heart disease;		
XX		cardiant; vasotropic; gene therapy.		
OS	Homo sapiens.			
PN	MO2003025152-A2.			
PD	27-MAR-2003.			
PF	23-SEP-2002; 2002MO-US030100.			
PR	21-SEP-2001; 2001US-0323816P.			
PA	(GENE-) GENE LOGIC INC.			
PA	(PROC) PROCTER & GAMBLE CO.			
PI	Einstein R, White M, Bednarik D, Greene J, Doersen C;			
DR	WPI; 2003-342664/32.			
DR	N-PSTDB; ABZ82228.			
PT	New isolated nucleic acid encoding a human secreted frizzled related			
PT	protein, useful for preparing a composition for treating ischemic heart			
PT	disease.			
PS	Claim 1; Page 49-50; 57pp; English.			
CC	The present sequence is the protein sequence of human secreted frizzled			
CC	related protein (sFRP). A variant sFRP protein (see ABP72783) has been			
CC	identified that is associated with ischemic heart disease. The variant			
CC	sequence differs from the present sequence in having Ala substituting for			
CC	Pro at position 114. The invention provides sFRP variant polypeptide,			
CC	vectors, host cells, and methods of producing the variant polypeptide.			
CC	The variant sFRP nucleic acids and polypeptides can be used to identify			
CC	agents which modulate the expression or activity of the polypeptide, to			
CC	identify binding partners for the protein, to raise antibodies, and as			
CC	diagnostic, prognostic and therapeutic agents for ischemic heart disease			
SQ	Sequence 314 AA;			
Query Match 53.4%; Score 924.5; DB 6; Length 314;				
Best Local Similarity 56.6%; Pred.No. 5.9e-90;				
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6				

PT New compositions comprising secreted frizzled related protein (SFRP),
PT anti-SFRP antibody, nucleic acid encoding SFRP or the antibody, or SFRP
PT antisense nucleic acids, for regulating bone-forming activity or treating
PT bone diseases.

Claim 24; SEQ ID NO 2; 57pp; English.

CC The invention relates to a pharmaceutical composition for regulating bone
CC -forming activity in a mammal comprising at least one a secreted frizzled
CC related protein (SFRP) or its regulating portion, an antibody against
CC such proteins, a nucleic acid that encodes for the protein or antibody,
CC an SFRP antisense nucleic acid, or a small molecule that has an effect on
CC any of the above. The pharmaceutical composition is useful for regulating
CC bone-forming activity in a mammal, or for treating a bone disorder in a
CC human, such as bone formation disorder, bone resorption disorder, a bone
CC density disorder or a degenerative bone disorder, such as an
CC osteoporosis, specifically type II osteoporosis. The present sequence
CC represents the amino acid sequence of the human secreted frizzled related
CC protein, SFRP-1.

CC
XX
SQ Sequence 314 AA;

Query Match 53.4%; Score 924.5; DB 8; Length 314;
Best Local Similarity 56.6%; Pred. No. 5.9e-90;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVTAALAL--LGAALHMAPRCEBYDYGMQAE--PLH-GRSYKPPQCLD 55
DB 1 MGIGSEGGRRGAAAGVLLALGALLAVGASBYDYVSQSDIGPQSGRFTYKPPQCLD 60
QY 56 IPADPLCHGVGYKMRLLPNLEHESLAENVKQOASWMLPLAKRGHSDTQVFLCSLFAV 115
DB 61 IPADRLCHNVGYKMRLLPNLEHETMAENVKQOASWVPLLNKCHAGTQVFLCSLFAV 120
QY 116 CLDRPIYPCRSICAEVVRAGCAFLMEAYGFPWPEMLHCHKFPDNDLCTAVQFGH-LPATA 174
DB 121 CLDRPIYPCRMICAEVVRAGCAFLMEAYGFPWPEMLHCHKFPDNDLCTAVQFGH-LPATA 179
QY 175 PPTVKICAGCEMEHSGADGLMEOMCSSDPVVKRIKIKIENGDRKLIAGOKKKLLKPGP 234
DB 180 PGGTIVPCPCDNLKSEALIEHLICASEFLRMKIKIKVKKENDKKIV--PKKKKPLKIGP 237
QY 235 LKRXDITKRLVLMKNGAGCCPCPDLSLGSFLVMGRKVDGQLLMAVYRMDKKNKMKFA 294
DB 238 IKKKDLKTLVLYLNKGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIRHMKDKKKEFKNF 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKKMKNHCEPPTQSVF 313

RESULT 13
ID ADR99142 standard; protein; 314 AA.
XX ADR99142;
XX 02-DEC-2004 (first entry)
DT Secreted frizzled-related protein 1, SFRP1, SEQ ID 148.
XX DE Secreted frizzled-related protein 1, SFRP1, SEQ ID 148.
XX KM Cytostatic; breast cancer; cancer; human;
XX Secreted frizzled-related protein 1; SFRP1.
XX Homo sapiens.
XX OS
XX PN WO2004078035-A2.
XX PD 16-SEP-2004.
XX PF 27-FEB-2004; 2004WO-US007268.
XX

PR 28-FEB-2003; 2003US-0450655P.

XX (FARB) BAYER PHARM CORP.
PA

XX Eweleigh D, Bigwood D;
PI

XX WPI; 2004-653556/63.
DR

XX N-PsDB; ADR99015.
DR

XX Diagnosing breast cancer comprises comparing the level of expression of
PT genes or gene products in a first biological sample taken from a patient
PT with that in a normal patient sample.

Claim 3; SEQ ID NO 148; 53pp; English.

CC The present invention relates to a method (M1) for diagnosing breast
CC cancer in a patient. The method comprises comparing the level of
CC expression of one or more genes or gene products in a biological sample
CC from the patient with that in a normal patient sample, where a difference
CC in the gene expression in the first sample compared to that in the second
CC sample is a diagnostic of the disease. Also claimed are: method (M2) for
CC distinguishing between normal and disease tissues; method (M3) for
CC monitoring the response of a breast cancer patient to treatment with an
CC anti-cancer agent; method (M4) for identifying a compound for treating
CC breast cancer; and an array for distinguishing between normal and disease
CC tissues comprising two or more probes corresponding to genes selected
CC from ADR98995-ADR99121 or comprising two or more polypeptides selected
CC from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995
CC -ADR99121 and the gene products are polypeptides selected from ADR99122-
CC ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are
CC useful for distinguishing between normal and disease tissue. M3 is useful
CC for monitoring the response of a breast cancer patient to treatment with
CC an anti-cancer agent. M4 is useful for identifying a compound for
CC treating breast cancer. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC
XX
SQ Sequence 314 AA;

Query Match 53.4%; Score 924.5; DB 8; Length 314;
Best Local Similarity 56.6%; Pred. No. 5.9e-90;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVTAALAL--LGAALHMAPRCEBYDYGMQAE--PLH-GRSYKPPQCLD 55
DB 1 MGIGSEGGRRGAAAGVLLALGALLAVGASBYDYVSQSDIGPQSGRFTYKPPQCLD 60
QY 56 IPADPLCHGVGYKMRLLPNLEHESLAENVKQOASWMLPLAKRGHSDTQVFLCSLFAV 115
DB 61 IPADRLCHNVGYKMRLLPNLEHETMAENVKQOASWVPLLNKCHAGTQVFLCSLFAV 120
QY 116 CLDRPIYPCRSICAEVVRAGCAFLMEAYGFPWPEMLHCHKFPDNDLCTAVQFGH-LPATA 174
DB 121 CLDRPIYPCRMICAEVVRAGCAFLMEAYGFPWPEMLHCHKFPDNDLCTAVQFGH-LPATA 179
QY 175 PPTVKICAGCEMEHSGADGLMEOMCSSDPVVKRIKIKIENGDRKLIAGOKKKLLKPGP 234
DB 180 PGGTIVPCPCDNLKSEALIEHLICASEFLRMKIKIKVKKENDKKIV--PKKKKPLKIGP 237
QY 235 LKRXDITKRLVLMKNGAGCCPCPDLSLGSFLVMGRKVDGQLLMAVYRMDKKNKMKFA 294
DB 238 IKKKDLKTLVLYLNKGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIRHMKDKKKEFKNF 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKKMKNHCEPPTQSVF 313

RESULT 14
ID ABB82244 standard; protein; 313 AA.
XX ABB82244;
XX

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 22:38:37 ; Search time 40 Seconds
(without alignments)
762.518 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730
Sequence: 1 MRAAAAGCVRTALALLG.....MFSYPSLYPPFYGAABPH 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1723	99.6	317	2	JB0175
2	614.5	35.5	295	2	JB0174
3	292.5	16.9	574	2	JB0339
4	277	16.0	581	2	S03540
5	268	15.5	581	2	UC7086
6	266.5	15.4	694	2	S71786
7	263.5	15.2	568	2	T25162
8	262.5	15.2	565	2	JB0338
9	262	15.1	647	2	JB0337
10	253.5	14.7	537	2	UC7127
11	247.5	14.3	641	2	A45054
12	243	14.0	550	2	T37325
13	206	11.9	666	2	UC7312
14	202	11.7	197	2	UC7735
15	198.5	11.5	605	2	T31690
16	191	11.0	706	2	JB0164
17	161	9.3	1113	2	JB0315
18	159.5	9.2	1774	2	B56101
19	134.5	7.8	579	2	UC7629
20	124	7.2	526	2	T13484
21	106	6.1	793	2	UC5539
22	91	5.3	327	2	F72482
23	90	5.2	1699	2	T14074
24	90	5.2	1906	1	S68235
25	89	5.1	583	2	JC6504
26	88	5.1	635	2	T46407
27	87	5.0	211	1	S45317
28	86	5.0	784	2	C82679
29	85.5	4.9	1050	2	T26395

30	85	4.9	465	2	S57564	nifB protein - Ent
31	84.5	4.9	1000	2	JB0110	mitotic control pr
32	84.5	4.9	1365	2	T13991	nucleoporin 154 -
33	84	4.9	713	2	UC2534	RVG protein - rat
34	84	4.9	763	2	T36248	CDA peptide synthe
35	83.5	4.8	211	2	UC4630	metalloproteinase
36	83.5	4.8	1513	2	T23681	hypothetical prote
37	82.5	4.8	211	1	A53532	hypothetical prote
38	82.5	4.8	902	2	B40494	androgen receptor
39	81.5	4.7	892	2	T15195	hypothetical prote
40	81.5	4.7	1322	2	D82685	phosphoribosylform
41	81.5	4.7	1349	2	T13031	nucleoporin - fru
42	81.5	4.7	1608	2	T13216	minor capsid prote
43	81	4.7	195	2	E82090	hypothetical prote
44	81	4.7	306	2	D82126	histone deacetylase
45	81	4.7	442	2	B31249	transforming growt

ALIGNMENTS

```
RESULT 1
JB0175
frizzled protein-1b - human
C:/Species: Homo sapiens (man)
C:/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:/Accession: JB0175
R;Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beely, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A;Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
A;Reference number: JB0174; MUID:98308108; PMID:9643118
A;Accession: JB0175
A;Molecule type: mRNA
A;Residues: 1-317 <HUA>
A;Cross-references: UNIPROT:O14780; UNIPARC:UP10000158811
C;/Genetic:
A;Gene: hFRP-1b
A;Map position: Sq14.3-q12.1

Query Match          99.6%; Score 1723; DB 2; Length 317;
Best Local Similarity 99.7%; Pred. No. 1.9e-147;
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAAAAGCVRTALALLGALHMAPARCEEYDYGMOAEPHAGRSYSKPPQCLDIPADL 60
DB 1 MRAAAAGCVRTALALLGALHMAPARCEEYDYGMOAEPHAGRSYSKPPQCLDIPADL 60
QY 61 PLCHTVGVYKRMRLPNLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAPVCLDRP 120
DB 61 PLCHTVGVYKRMRLPNLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAPVCLDRP 120
QY 121 ITPCRSLCAVYAGCAPLMEAGFPWPEMLHCHKRPPLNDLCIANVOFGHLPPTAPPVTKI 180
DB 121 ITPCRSLCAVYAGCAPLMEAGFPWPEMLHCHKRPPLNDLCIANVOFGHLPPTAPPVTKI 180
QY 181 CAQCEWESADGLMEOWCSSDFVVKRIKEIKTEGDRKLGAQKKQLLKGPPLKRDY 240
DB 181 CAQCEWESADGLMEOWCSSDFVVKRIKEIKTEGDRKLGAQKKQLLKGPPLKRDY 240
QY 241 KRLVLMKNGAGCCPQDLISLAGSFLVMGRKVDGQLLMAVYRWDMKMKFAVKFMS 300
DB 241 KRLVLMKNGAGCCPQDLISLAGSFLVMGRKVDGQLLMAVYRWDMKMKFAVKFMS 300
QY 301 YPCSLTYPPFYGAABPH 317
DB 301 YPCSLTYPPFYGAABPH 317

RESULT 2
JB0174
frizzled protein-2 - human
C:/Species: Homo sapiens (man)
C:/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
```

C/Accession: J01174
R/Hu_E; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A/Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas
A/Reference number: J01174; MUID:98508108; PMID:9642118
A/Accession: J01174
A/Molecule type: mRNA
A/Residues: 1-295 <HUA>
A/Cross-references: UNIPROT:Q9HAF5; UNIPARC:UPI000004BEB9
C/Genetics:
/Map position: 4q

	Query Match	35.5%;	Score 614.5;	DB 2;	Length 295;
	Best Local Similarity	43.9%;	Pred. No. 1.2e-47;		
	Matches	126;	Conservative	50;	Mismatches 94; Indels 17; Gaps 7;
Qy	14	ALALLLGAHPARCEETDYDGWDAEPLHGRSRSSKPPQCLDIPADPLCHTVGYKMR	73		
Db	7	SLLLFLASHCCIGASARGLFLLG-QPDSYRSNCKP-----IPANIQLCHGIEYQNMRL	60		
Qy	74	PNLEHESIAEVKQOASGMLPLAKRCHSDPQVFLCSLFAPVCC--LDRPIYPSRISCEA	130		
Db	61	PNLLGHETMEKVELDQAGMIRLVKMGCHPDITKFKLCSFAVLCDDIDDEITIQPHSLCYQ	120		
Qy	131	VRACGAPLMEYGGPRPPEMLHGHKFPRLDNDLCIAVQGH--LPAT--APRYTKCAQCEM	186		
Db	121	VKDCAPMWSAFGGPPMDLPCDRFPQDNDICIPASSDHLPLPAETEP--KYCEACKN	177		
Qy	187	EHSADG-LMEQMSSDFVVKRIKEIKIENGDRKLIGAOKKKLLKGPRLKRXDKTKLV	245		
Db	178	KNDDNDIMETLCNDDPALTKIKVEIITYINDTKIILETTSKTIYKLVNGSERLRKSVL	237		
Qy	246	HMKRGAGCPQQLDSLAGSLVMGRKVDGQLLAIVRYRDKKEMK	292		
Db	238	WLKSLQCTCEENNINAPYLMGQKOGELVITTSYVKRWQGGQEFK	284		

Query March	16.9%	Score 292.5;	DB 2;	Length 574;
Best Local Similarity	38.9%	Pred. No. 2.4e-16;		
Matches 65;	Conservative 22;	Mismatches 63;	Indels 17;	Gaps 5;

Qy	3	AAAAAGGRTAALV-LIGALHWA	PARCEEDYQWQAEPLHG-RSYSKPEQCLIDPADL	60
Db	6	AAALPLSSIGLALVIALIGALS-----	AGAGQPYHGRKGISVPHGFCQPRISI	54
Qy	61	PLCHTVGYKRMRLPNLLEHESLAEVYKQ	ASSWMLPLAKRCHSDPQVPLCSLFAFVLC--LD	118
Db	55	PLCTDIAVNGTILPRLTGHGTNQEDAGLE	VHQFYPLVKVQCSPELIRFLFCSMYAVPVCITLD	114
Qy	119	RPIYPCRSLECAVNAVAGCAPLMEAVG	FPPWBPMLHCHKFPLD--NDLCT	163
Db	115	QAIPRCRLCERARQGCALNNKGFQW	PEPLRCGNFVHGAGELCV	161

gene frizzled protein precursor - Fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #ext_change 09-Jul-2004
C/Accession: S03540; S15708; S15709
R/Vinson, C.R.; Conover, S.; Adler, P.N.
Nature 338, 263-264, 1989
A/Title: A *Drosophila* tissue polarity locus encodes a protein containing seven potential
A/Reference number: S03540; PMID:89159415; PMID:2493563
A/Accession: S03540
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-581 <VAV>

[illegible]


```

C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001
C:Accession: J07312
R:Salu, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.
R:Saia, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.
R:Saia, C.F.; Formenti, E.; Terstappen, G.C.; Caricasole, A.
A:Title: Identification, gene structure, and expression of human frizzled-3 (FZD3).
A:Reference number: J07312
A:Accession: J07312
A:Molecule type: mRNA
A:Residues: 1-666 <Sal>
A:Cross-references: UNIPARC:UPI0000178F62; GB:AJ277242
A:Experimental source: brain
C:Comment: This protein, a seven-transmembrane receptor belonging to the frizzled family,
nostol levels in cells.
C:Genetics:
A:Gene: fz3
A:Map position: 8p21
C:Superfamily: fruit fly frizzled protein
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match          11.9%  Score 206;  DB 2;  Length 666;
Best Local Similarity 36.3%  Pred. No. 1.7e-10;
Matches 37;  Conservative 18;  Mismatches 45;  Indels 2;  Gaps 1;

Qy      57 PADLPLCHTVGYSKRMRLPNLLLEHESLAEVKKQOASWLPDLAKRCHSDTQVFLCSLFAFVC 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      30 PFTLMQCDDLRYNTFTFMNLNTHYDQFALALAMEPFHVMVNDICSDRDRPFLCALYAPIC 89

Qy      117 LD--RPIYPCRSICAVNAGCAPILMEAGFPMPEMLHCHKRP 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      90 MEYGRVTLPCRRLCORAYSECSKLEMFGEVPMPEMDECSRFP 131

```

```
CjDate: 29-Oct1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001
CjAccession: T31690
RjNameley, P.; Keppler, D.
A:Description: The sequence of C. elegans cosmid F27E11.
A:Reference number: Z21069
A:Accession: T31690
A>Status: preliminary; translated from GB/EWBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-605 <MAM>
A:Cross-References: UNIPARC:UPI0000178F63; EMBL:AF016413; PIDN:AAB55257.1; GSPDB:GN00023
A:Experimental source: strain Bristol N2; clone F27E11
CjGene: CESP:F27E11.3
A:Map position: 5
A:Introns: 28/3; 454/1; 520/1; 562/1
CjSuperfamily: fruit fly frizzled protein

Query Match      11.5%; Score 198.5; DB 2; Length 605;
Best Local Similarity 37.0%; Pred. No. 7.3e-10;
Matches 40; Conservative 16; Mismatches 45; Indels 7; Gaps 3;

QY      74 PNLEHSLAEVQGQASMTPLAKCHSDPTGFLCSLPAPVC---LDRIYFCRSLSCEA 130
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       5 PNTSGHKQKQBAGLEVHQGFYPLVEVGCFGLKFFLCMTYPIQENYDKIILCEMLQVE 64

QY      131 VRAGACALMEAYGFPWEEMLCHKRPFLDNDLCIAVOFGHLPATAPVT 178
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      65 ARSKCSIMAKYGFRWPETLSCEALPMGD---QMSTGNICA-APDPT 108
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Search completed: March 22, 2006, 22:43:02
Job time : 41 secs

Search completed: March 22, 2006, 22:43:02
Job time : 41 secs

```

RESULT 14
JC7735
frizzled-related protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Dec-2001
Accession: JC7735
Revision: 14-Dec-2001 #text_change 09-Jul-2004
R:Yam, J.W.P.; Chan, K.W.; Wong, V.K.W.; Hsiao, W.L.W.
Biochem. Biophys. Res. Commun. 286, 94-100, 2001
A:Title: Transcriptional activity of the promoter region of rat frizzled-related protein
A:Reference number: JC7735; MUID:21378144; PMID:11485313
A:Accession: JC7735
A:Molecule type: DNA
A:Residues: 1-197 <YAM>
A:Cross-references: UNIPROT:O9UIS5; UNIPARC:UPI000017CBB3; GB:AF140347
C:Comment: This protein is a new family of secreted proteins involved in tumorigenesis &
C:Genetics:
A:Gene: rFrp
A:Introns: 148/3; 175/3

Query Match      11.7%  Score 202; DB 2; Length 197;
Beat Local Similarity 27.5%  Pred. No. 1e-10;
Matches 49; Conservative 27; Mismatches 76; Indels 26; Gaps 3;

Dd      60  LP LCHTVGYKRRRLPNLLIEHSLAEVKKQASSWLFPLAKRGHSDTQVFLGSLFAPVC-- 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      29  IPMCRRMPMNITRMBNHLHSTQENAILAIGQYELVDVNCSSVLSFPLCAMYAPICLLE 88
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      117 -LDRITYRCRSLCEAVRAGCAPLMEAYGFPPEMLCHKFLP-DNDLCIAVQFGHLPRATA 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      89  FLHPDPKCKSKVCCQARDDCEPLMKMYNHSWPESLACDELPYDRGVCIS----- 138
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RESULT 15
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hypothetical protein F27B1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

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